

## SEQUENCE LISTING

<110> Genentech, Inc.  
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<120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

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<140> 09/665,350  
<141> 2000-09-18

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<212> PRT

<213> Homo sapiens

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65 70 75 80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala  
85 90 95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr  
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Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys  
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Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser  
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Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
 145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
 165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
 245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
 290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
 305 310 315 320

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Leu

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<211> 2206

<212> DNA

<213> Homo sapiens

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aacagccctg gctgaggggag ctgcagcgca gcagagtatac tgacggcgcc aggttgcgtta 180

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<213> Homo sapiens

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln			
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Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly			
100		105	110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro			
115		120	125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
130		135	140
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu			
145		150	160
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
165		170	175
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
180		185	190
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His			
195		200	205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys			
210		215	220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
225		230	240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys			
245		250	255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
260		265	270
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
275		280	285
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu			
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Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys			
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His Glu Pro Asn Lys Cys Gln Cys Glu Gly Trp His Gly Arg His			
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Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala			
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<212> DNA

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<212> DNA

<213> Artificial Sequence

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<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 11
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<212> DNA
<213> Homo sapiens

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<211> 164

<212> PRT

<213> Homo sapiens

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Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
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Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
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Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
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Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
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Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
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<210> 13  
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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe  
  
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 <210> 17  
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 <210> 18  
 <211> 189  
 <212> PRT  
 <213> Homo sapiens

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													25	30	

Pro	Pro	Ser	Leu	Arg	Cys	Ser	Leu	His	Ser	Ala	Cys	Cys	Ser	Gly	Asp
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Pro	Ala	Ser	Tyr	Arg	Leu	Trp	Gly	Ala	Pro	Leu	Gln	Pro	Thr	Leu	Gly
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Val	Val	Pro	Gln	Ala	Ser	Val	Pro	Leu	Leu	Thr	Asp	Leu	Ala	Gln	Trp
													65	70	80

Glu	Pro	Val	Leu	Val	Pro	Glu	Ala	His	Pro	Asn	Ala	Ser	Leu	Thr	Met
													85	90	95

Tyr	Val	Cys	Thr	Pro	Val	Pro	His	Pro	Asp	Pro	Pro	Met	Ala	Leu	Ser
													100	105	110

Arg	Thr	Pro	Thr	Arg	Gln	Ile	Ser	Ser	Ser	Asp	Thr	Asp	Pro	Pro	Ala
													115	120	125

Asp	Gly	Pro	Ser	Asn	Pro	Leu	Cys	Cys	Cys	Phe	His	Gly	Pro	Ala	Phe
													130	135	140

Ser	Thr	Leu	Asn	Pro	Val	Leu	Arg	His	Leu	Phe	Pro	Gln	Glu	Ala	Phe
													145	150	160

Pro	Ala	His	Pro	Ile	Tyr	Asp	Leu	Ser	Gln	Val	Trp	Ser	Val	Val	Ser
													165	170	175

Pro	Ala	Pro	Ser	Arg	Gly	Gln	Ala	Leu	Arg	Arg	Ala	Gln			
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&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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24

&lt;210&gt; 20

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&lt;212&gt; DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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 gagtgagaag tacatctgta tgaacaagag gggcaagtc atcgggaagc ccagcggaa 360  
 gagcaaaagac tgcgtttca cggagatcgt gctggagaac aactatacgg ctttcagaa 420  
 cgcccgccac gagggtctgg tcatggcctt cacgcggcag gggggcccc gccaggttc 480  
 cccgagccgc cagaaccaggc gggaggccca cttcatcaag cgcctctacc aaggccagct 540  
 gcccctcccc aaccacgccc agaagcagaa gcagttcgag tttgtggct ccgccccccac 600  
 cccggccgacc aagcgcacac ggcggccca gcccctcaag tagtctggga ggcaggggc 660  
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 cccagctggg aaggggcagg cccgtcccc agggggcggt ggcacagtgc ccccttcccg 840  
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 ccccagcccc caaactcctc ctggctagac tgttaggaagg gacttttgtt tggttgtt 1080  
 tttcaggaaa aaagaaaagg agagagagga aaatagaggg ttgtccactc ctcacattcc 1140  
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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23  
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Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 24

cagtagtga gggaccaggg cgccatga

28

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gcca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
 gggatctgc cgccctgctca nctggtcggc catggcgccc t 41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
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 aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120  
 ttaccatacg ccctcaggac gttccctcta gctggagtcc tgacttcaa cagaacccca 180  
 tccagtcatt ttgattttgc tgtttatttt tttttcttt ttcttttcc caccacattt 240  
 tattttattt ccgtacttca gaaatggcc tacagaccac aaagtggccc agccatgggg 300  
 ctttttctt gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
 tcctggctg cccttagtgtg tgccgctgctg acaggaactt tgtctactgt aatgagcgaa 420  
 gttgacetc agtgcctctt gggatcccgg agggcgtaac cgtactctac ctccacaaca 480  
 accaaattaa taatgcttga tttctgcag aactgcacaa tttacagtctg gtgcacacgg 540  
 tctacctgtt tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600  
 ttctccattt gcaggaaaaac aatattcaga ccatttcacg ggctgctctt gcccagctct 660  
 tgaagcttga agagctgcac ctggatgaca actccatatac cacagtgggg gtggaaagacg 720  
 gggccttccg ggaggctatt agcctcaaattt ttttttttgc ttcttgc 780  
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gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560  
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gtgagaagca acacctgago ctggtaact tagagccccg atccacctat cggattttgtt 1740  
tagtgcacact ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800  
ccacccatgc ctccatctg aacaacggca gcaacacagc gtccagccat gaggcagacga 1860  
cgccccacag catgggctcc ccctttctgc tggegggctt gatcgaaaaaa gggcgctaca 1920  
tttgtcttgtt ggttttgc acgttctttt gctggcatat gcacaaaaaaag gggcgctaca 1980  
cctcccaagaa gtggaaataac aaccggggcc ggccggaaaga tgattattgc gaggcaggca 2040  
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ataacgatca actccttaaa ggagattca gactgcagcc catttacacc ccaaattgggg 2160  
gcattaatta cacagactgc catatccccca acaacatgog atactgcaac agcagcgtgc 2220  
cagacctgga gcaactgccat acgtgacacgc cagaggccca gcgttatcaa ggcggacaat 2280  
tagactcttgc agaacacact cgtgtgtca cataaaagaca cgcagattac atttgataaa 2340  
tgttacacag atgcatttgtt gcatttgaat actctgtat ttatacgggt tactatataa 2400  
tgggatttaa aaaaagtgtt atctttctt tttcaagttt attacaaaaca gttttgttaac 2460  
tctttgtttt taaaatctt 2479

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu

1                    5                    10                    15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys  
20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
 35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
                   85                   90                   95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
           100                 105                 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
                   115                  120                  125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405	410	415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val		
420	425	430
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met		
435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
660		
<210> 29		
<211> 21		
<212> DNA		

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggtctacct gtagggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

aacgagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctttgcc agctttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttggagca agcggcgccg gcggagacag aggcagaggc agaagctggg gctccgtcct 60  
cgcccccac gagcgatccc cgaggagagc cgccggccctc ggcgaggcga agaggccgac 120

gaggaaagacc cgggtggctg cgccctgcc tcgcttcca ggcgcggcg gctgcaccc 180  
 tgccccttt gctgccttg aaaatggaaa agatgctcg aggctgttt ctgcgtatcc 240  
 tcggacagat cgtccttcctc cctgcccagg ccaggagcg gtacacgtggg aggtccatct 300  
 ctagggcag acacgctcg accacccgc agacggccct tctggagagt tctgtgaga 360  
 acaagcgggc agacctggtt ttcattcatcg acagctctcg cagtgtcaac acccatgact 420  
 atgcaaaggta caaggagttc atcgtggaca tcttgcattt ctggacatt ggteetgatg 480  
 tcacccgagt gggcctgctc caatatggca gcactgtcaa gaatgagttc tccctcaaga 540  
 ccttcaagag gaagtcggag gtggagcgtg ctgtcaagag gatgcggcat ctgtccacgg 600  
 gcaccatgac tgggctggcc atccatgtt ccctgaacat cgattctca gaagcagagg 660  
 gggccggcc cctgaggag aatgtgccac gggtcataat gatcgtgaca gatggagac 720  
 ctcaggactc cgtggccggag gtggctgcta aggacacggga cacgggcatc ctaatcttg 780  
 ccattggtgtt gggccaggtt gacttcaaca ccttgaagtc cattggagt gagccccatg 840  
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 agaagaaggta gtgcacggcc cacatgtgca gcacccctgga gcataactgt gcccacttct 960  
 gcatcaacat ccctggctca tacgtctgca ggtgcaaaaca agctacatt ctcaactcg 1020  
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 atcaatgcaa atgtgaaaac cttataatgt tccagaacct tgcaaacgaa gaagtaagaa 2880  
 aattaacaca ggcgttagaa gaaatgacac agagaatggaa agccctggaa aatcgccctga 2940  
 gatacagatg aagattagaa atcgcacac atttgttagtc attgtatcac ggattacaat 3000  
 gaacgcgtg cagagccccaa aagctcaggc tattgttaaa tcaataatgt tggaaatggaa 3060  
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 catcctgcct tagtgcata tctcatttgcata ctatacgata aagtttgcac agtcttactt 3300

ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatata 3360  
 gtatatggat gtatgcataa aatcatagga catatgtact tgtggaacaa gttggattt 3420  
 ttatacaata taaaattca ccacttcag 3449

<210> 34  
 <211> 915  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile  
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 Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30  
 Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45  
 Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60  
 Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80  
 Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95  
 Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110  
 Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125  
 His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140  
 Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160  
 Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175  
 Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190  
 Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205  
 Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220  
 Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245		250	255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260		265	270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275		280	285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290		295	300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305		310	315
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325		330	335
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340		345	350
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355		360	365
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370		375	380
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385		390	395
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405		410	415
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420		425	430
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435		440	445
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450		455	460
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465		470	475
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485		490	495
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500		505	510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590  
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655  
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720  
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735  
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780  
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
 805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
 820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
 835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
 850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
 865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
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Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
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Arg Tyr Arg  
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<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 36

acagccatgg tctatacgctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

&lt;210&gt; 38

&lt;211&gt; 1813

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

ggagccgccc tgggtgtcag cggcteggtc cccgcgcacg ctccggccgt cgcgcagcct 60  
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 ggctgagtgc cctcgcgcgc ccctcgcggc cccagctgca actgcacttg cccgcacaacc 240  
 ggttgcaggc ggtggagggg gggaaagtgg tgcttccagc gtggtagcacc ttgcacgggg 300  
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 tttgtatgaa aaa 1813

&lt;210&gt; 39

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

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Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln			
20	25	30	
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val			
35	40	45	
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln			
50	55	60	
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys			
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Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro			
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Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg			
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Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val			
115	120	125	
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
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Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
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Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275	280	285	

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
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Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
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Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
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Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
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Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
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Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

agggtctcca ggagaaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

atttgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42  
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 43  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 43  
gtgtgacaca gcgtgggc 18

<210> 44  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 44  
gaccggcagg cttctgcg 18

<210> 45  
<211> 25  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 45  
cagcagcttc agccaccagg agtgg 25

<210> 46  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 46  
ctgagccgtg ggctgcagtc tcgc 24

<210> 47

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<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 47
ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
<211> 2822
<212> DNA
<213> Homo sapiens

<400> 48
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aa						2822

<210> 49

<211> 690

<12> PRT

<213> Homo sapiens

<400> 49

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20 25 30

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn  
50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly  
65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln  
85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn  
           100                 105                 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys  
                   115                  120                  125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln  
 130 135 140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile  
 145 150 155 160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys  
                   165                  170                  175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
 465 470 475 480  
 Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
 485 490 495  
 Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
 500 505 510  
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 Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
 530 535 540  
 Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
 545 550 555 560  
 Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
 565 570 575  
 Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
 580 585 590  
 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
 595 600 605  
 Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
 610 615 620  
 Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
 625 630 635 640  
 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
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 Gly Met Phe Ile Phe Leu Phe Cys Val Leu Ser Arg Lys Ile Gln  
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 Leu Arg  
 690

<210> 50  
 <211> 589  
 <212> DNA  
 <213> Homo sapiens  
  
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 <222> (61)

<223> a, t, c or g

<400> 50

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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 52

ggagtagaaa gcgcattgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54  
cgagctcgaa ttaattcg 18

<210> 55  
<211> 18  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 55  
ggatctcctg agctcagg 18

<210> 56  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 56  
ccttagttgag tgatccttgt aag 23

<210> 57  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 57  
atgagaccca cacctcatgc cgctgtatac acctgacaca ttttgcaatt 50

<210> 58  
<211> 2137  
<212> DNA  
<213> Homo sapiens

<400> 58  
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 ggcagttct gtcatggatg ctgtcctgag aataacttgc tgtcccggtg tcacctgtt 1800  
 ccatctccca gcccaccagc cctctgcaca ctcacatgc ctcccatgg attggggcct 1860  
 cccaggcccc ccacctttagt tcaacactgca cttctgttc aaaaatcagg aaaagaaaaag 1920  
 attgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagaccta 1980  
 gaacccttcc caagcaactt ggtttccaa catgatattt atgagtaatt tattttgata 2040  
 tgtacatctc ttatttctt acattattt tgccccaaa ttatatttat gtatgtaaat 2100  
 gagtttgtt ttgtatatta aatggagtt tgtttgt 2137

&lt;210&gt; 59

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

Met	Arg	Ser	Gly	Cys	Val	Val	Val	His	Val	Trp	Ile	Leu	Ala	Gly	Leu
1					5			10			15				

Trp	Leu	Ala	Val	Ala	Gly	Arg	Pro	Leu	Ala	Phe	Ser	Asp	Ala	Gly	Pro
20						25						30			

His	Val	His	Tyr	Gly	Trp	Gly	Asp	Pro	Ile	Arg	Leu	Arg	His	Leu	Tyr
35						40						45			

Thr	Ser	Gly	Pro	His	Gly	Leu	Ser	Ser	Cys	Phe	Leu	Arg	Ile	Arg	Ala
50						55						60			

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205

Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 60

atccgccccag atggctacaa tgtgtta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 61

gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 62  
ccagtccggt gacaagcccc aa

22

<210> 63  
<211> 1295  
<212> DNA  
<213> Homo sapiens

<400> 63  
cccagaagtt caaggcccc cggcctcctg cgctcctgcc gccgggaccc tcgaccctcct 60  
cagagcagcc ggctgcggcc ccgggaagat ggcgaggagg agccgcacc gcctcctcct 120  
gtgtgtgtcg cgctacotgg tggctgcctt gggctatcat aaggcctatg gttttctgc 180  
cccaaaagac caacaagtag tcacagcagt agactaccaa gaggctattt tagcctgcaa 240  
aaccccaaag aagactgttt cctccagatt agagtgaag aaactgggtc ggagtgtctc 300  
ctttgtctac tatcaacaga ctcttcaagg tgatttaaa aatcgagctg agatgataga 360  
tttcaatatac cggatcaaaa atgtgacaag aagtgtatgcg gggaaatatac gttgtgaagt 420  
tagtgccca tctgagcaag gccaaaacctt ggaagaggat acagtcaactc tggaaagtatt 480  
agtggctcca gcagttccat catgtgaagt acccttctt gctctgagtg gaactgtgg 540  
agagctacga tgtcaagaca aagaaggaa tccagctcct gaatacacat gtttaagga 600  
tggatccgt ttgctagaaa atccccactt tggctccaa agaccaaca gctcatacac 660  
aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720  
atattctgt gaagcccgca attctgttgg atatcgagg tgcctggaa aacgaatgca 780  
agtagatgtatcataa gtggcatcat agcagccgtt gtagttgtgg ccttagtgat 840  
ttccgttgtt ggccttgggtg tatgttatgc tcagaggaaa ggctactttt caaaagaaac 900  
ctccttccag aagagtaatt cttcatctaa agccacgaca atgagtgaaa atgtgcagtg 960  
gttcacgcct gtaatcccgac cactttggaa ggcgcggcg ggcggatcac gaggtcagga 1020  
gttctagacc agtctggcca atatggtaa accccatctc tactaaaata caaaaattag 1080  
ctggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
acccggggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcctt gctggtaa 1200  
cagagcaaga ttccatctca aaaaataaaaa taaataata aataaaataact gtttttacc 1260  
tgttagaaatc ttacaataaa tatacgatc tattc 1295

<210> 64  
<211> 312  
<212> PRT  
<213> Homo sapiens

<400> 64  
Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
                  35                        40                        45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
                  50                        55                        60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
        65                            70                        75                        80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
                  85                        90                        95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
                  100                        105                        110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
                  115                        120                        125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
                  130                        135                        140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
                  145                        150                        155                        160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
                  165                        170                        175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
                  180                        185                        190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
                  195                        200                        205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
                  210                        215                        220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
                  225                        230                        235                        240

Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
                  245                        250                        255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
                  260                        265                        270

Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
                  275                        280                        285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
                  290                        295                        300

Gly Gly Ser Arg Gly Gln Glu Phe

305 310

<210> 65  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 65 22  
atcgttgtga agttagtgcc cc

<210> 66  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 66 23  
acctgcgata tccaacagaa ttg

<210> 67  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 67 48  
ggaagaggat acagtcaactc tggaagtatt agtggctcca gcagttcc

<210> 68  
<211> 2639  
<212> DNA  
<213> Homo sapiens

<400> 68  
gacatcgag gtgggcttagc actgaaaactg cttttcaaga cgaggaagag gaggagaaaag 60  
agaaaagaaga ggaagatgtt gggcaacatt tatttaacat gctccacagc ccggaccctg 120  
gcatcatgct gctattccctg caaatactga agaaggcatgg gatttaaata ttttacttct 180  
aaataaatga attactcaat ctcctatgac catctataca tactccacct tcaaaaagta 240  
catcaatatt atatcattaa ggaatatgta accttctctt ctccaatatg catgacattt 300  
ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360  
tggcattcatt catttgacaa atgcaagcat cttccttatac aatcagctcc tattgaactt 420  
actagcactg actgtggaat ccttaagggc coattacatt tctgaagaag aaagctaaga 480  
tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagta 540

aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaatac aggccctgg 600  
 ttacacccag atccatttat atggaagcat ctacagtgg a ttgtaatgat ttaggtctt 650  
 taactttccc agccagattg ccagctaaca cacagattct tcctctacag actaacaata 720  
 ttgcaaaaat tgaatactcc acagacttc cagtaaacct tactggcctg gatttatctc 780  
 aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctca gtccttctg 840  
 tgtacctaga ggaaaacaaa cttactgaac tgccctgaaaa atgtctgtc gaactgagca 900  
 acttacaaga actctatatt aatcacaact tgctttctac aatttcaccc ggagcctta 960  
 ttggcctaca taatcttctt cgacttcato tcaattcaaa tagattgcag atgatcaaca 1020  
 gtaagtgggt tgatgctctt ccaaatactag agattctgtat gattggggaa aatccaatta 1080  
 tcagaatcaa agacatgaac tttaaggctc ttatcaatct tcgcagcctg gttatagctg 1140  
 gtataaacct cacagaaata ccagataacg cttgggtgg actggaaaac ttagaaagca 1200  
 tctctttta cgataacagg cttattaaag taccctatgt tgctcttcaa aaagtgtaa 1260  
 atctcaaattt ttggatcta aataaaaatc ctattaatag aatacgaagg ggtgattta 1320  
 gcaatatgct acactaaaaa gagttgggaa taaataatat gcctgagctg attccatcg 1380  
 atagtctgc tggataac ctgcaggatt taagaaaaat agaagctact aacaacccta 1440  
 gattgtctt cattcaccccc aatgcattt tcagactccc caagctggaa tcactcatgc 1500  
 tgaacagcaa tgctctcagt gcccgttacc atggtaaccat tgagtctctg ccaaaccctea 1560  
 agggaaatcag catacacagt aaccccatca ggtgtgactg tgcattccgt tggatgaaca 1620  
 tgaacaaaac caacattcga ttcatggago cagattcact gtttgcgtg gacccacctg 1680  
 aattccaagg tcagaatgtt cggcaagtgc atttcaggaa catgatggaa atttgcctcc 1740  
 ctcttatagc tcctgagagc ttccattcta atctaaatgt agaagctggg agctatgtt 1800  
 ccttcactg tagagctact gcagaaccac agcctgaaat ctactggata acacccctg 1860  
 gtcaaaaact cttgcctaatt accctgacag acaagttcta tgccattct gaggaaacac 1920  
 tagatataaa tggcgtaact cccaaagaag gggtttata tacttgtata gcaactaacc 1980  
 tagttggcgc tgacttgaag tctgttatga tcaaagtgg tggatctttt ccacaagata 2040  
 acaatggctc ttgaatatt aaaataagag atattcaggc caattcagtt tgggtgcct 2100  
 ggaaagcaag ttctaaaatt ctcaaatcta gtgttaatg gacagcctt gtcaagactg 2160  
 aaaattctca tgctgcgcaa agtgcctgaa taccatctga tgtcaaggta tataatctta 2220  
 ctcatctgaa tccatcaact gaggataaaa ttgttatgat tattccacc atctatcaga 2280  
 aaaacagaaa aaaatgtgt aatgtcacca ccaaaggtt gcacccctgat caaaaagagt 2340  
 atgaaaagaa taataccaca acacttatgg cctgtcttg aggccctctg gggattattg 2400  
 gtgtgatatg tcttatacgc tgccctctc cagaaatgaa ctgtgatgg ggacacagct 2460  
 atgtgaggaa ttacttacag aaaccaaccc ttgcatttagg ttagctttat ctcctctga 2520  
 taaatctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtt 2580  
 taggttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

<210> 69  
 <211> 708  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
 Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile  
 1 5 10 15

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu  
 20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
 35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
 50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
560		
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
 625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
 645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
 660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
 675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
 690 695 700

Thr Asn Met Ser  
 705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

gccccggact ggcgcaaggt gcccaagcaa ggaaagaaaat aatgaagaga cacatgtgtt 60  
 agctgcagcc ttttgaaca cgcagaagg aaatcaatag tggacagg gctggAACCT 120  
 ttaccacgct tggagata gatgaggaat gggctcgta ttatgctgac attccagcat 180  
 gaatctggta gacctgtgtt taacccgttc cctctccatg tgcctctcc tacaaagttt 240  
 tggtttatg atactgtgtt ttcattctgc cagtatgtgt cccaggcgt gtctttgttc 300  
 ttcctctggg ggttaaatg tcacctgttag caatgcaaat ctcaaggaaa tacctagaga 360  
 tcttcctcct gaaacagtct tactgtatct ggactccaat cagatcacat ctattccaa 420  
 tgaaattttt aaggacctcc atcaacttag agttctcaac ctgtccaaaa atggcattga 480  
 gtttatacgat gagcatgcct tcaaaggagt agctgaaacc ttqcaqactc tggacttgc 540  
 cgacaatcg attcaaagtg tgccaaaaaa tgccttcaat aacctgaagg ccagggccag 600  
 aattgccaac aacccttggc actgcactg tactctacag caagttctga ggagcatggc 660  
 gtccaatcat gagacagccc acaacgtat ctgtaaaacg tccgtgttg atgaacatgc 720  
 tggcagacca ttccctcaatg ctgccaacga cgctgacctt tgcacccatcc ctaaaaaaaaac 780  
 taccgattat gccatgtgtt tcacccatgtt tggctgttgc actatggta tctcatatgt 840  
 ggtatattat gtgaggccaa atcaggagga tgcccgaga cacctcgaat acttgaatc 900  
 cctgccaagc aggacagaaga aagcagatga acctgtatgat attagcactg tggatagtg 960  
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 ggtttaatcc tcccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgaat 1080  
 tatgccactg ctgaactttt aacaaacact acaacataaa taatttgagt ttaggtgatc 1140  
 cacccttaa ttgtaccccc gatggatat ttctgagtaa gctactatct gaacatttagt 1200  
 tagatccatc tcactatatta ataatgaaat ttatTTTTT aatttaaaag caaataaaag 1260  
 cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Gly Gly Leu Asn Val  
 35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255

Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

accgagcnga gcggaccgaa ggcgccgcgg agatgcaggt gagcaagagg atgctggcgg 60  
 gggcggtggag gggcatgccc agccccctcc tggcctgctg gcaagccatc ctccctgctgg 120  
 tgcgtggcgtc agtgcgtgtca ggctcgccca cgggctgccc gcccccgtgc gagtgctccg 180  
 cccaggaccc cgctgtgtcg tgccaccgca agtgcttgc ggcagtcccc gagggcatcc 240  
 ccacccgagac ggcgcgtgtcg gacctaggca agaacccgtc caaaaacgctc aaccaggacg 300  
 agttgcgcag cttccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgcgg 360  
 tggagccggg cgcccttcac aaccttca acctccggac gctgggtctc cgcagaacc 420  
 ggcgtgaagct catcccgcta ggcgttca ctggccctcg caacctgacc aagcaggaca 480  
 tcagcggagaa caagatcggtt atcctactgg actacatgtt tcaggacgtg tacaacctca 540  
 agtcactggaa ggttggcgac aatgacactcg tctacatctc tcaccgcgc ttcagcggcc 600  
 tcaacagect ggagcagctg acgctggaga aatgcaaccc gacctccatc cccaccggagg 660  
 cgctgttcacca cctgcacggc ctcatcggtcc tgaggctccg gcacctcaac atcaatgcac 720  
 tccgggacta ctcccttcac aggctgtacc gactcaaggt ctggagatc tcccactggc 780  
 cctacttggaa caccatgaca cccaactgac tctacggcct caacctgacg tccctgtcca 840  
 tcacacactg caatctgacc gctgtgcctt acctggccgt ccggccaccta gtctatctcc 900  
 gettccttcac aaccccatca gcaccattga gggctccatg ttgcattgac 960  
 tgcgtccggctc gcaggagatc cagctggtgg gggggcagct gggcgtgggt gggccctatg 1020  
 cctcccgccgg cctcaactac ctgcgcgtgc tcaatgtctc tggcaacccag ctgaccacac 1080  
 tggaggaatc agtcttccac tgggtggca acctggagac actcatctg gactccaacc 1140  
 cgctggccgtc cgactgtcggt ctccctgtggg tggccggcgg ccgcgtggcgg ctcaacttca 1200  
 accggcgtca gcccacgtgc gccacgcccgg agtttgcata gggcaaggag ttcaaggact 1260  
 tccctgtatgt gctactgccc aactacttca cctgcgcgtgc cggccgcata cgggaccgca 1320  
 aggccccagca ggtgtttgtg gacgaggggcc acacgggtca gtttgtgtgc cgggcccattg 1380  
 gcaaccgcgc gcccgcata ctctggctc caccggaaa gcacctggtc tcagccaaga 1440  
 gcaatggcgc gtcacatgc ttccctgtatgc gacgcgtggaa ggtgcgttac gcccaggtac 1500  
 aggacaacgg cacgtacctg tgcatcgccgg ccaacgcggg cggcaacgac tccatgcgg 1560  
 cccacctgtca tgtgcgcgcg tactcgccca actggccca tcagcccaac aagaccttcg 1620  
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 ggaccccccacc tacacagggg cattgacaga ctggaggta aagccgacga accgacacgc 2160  
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 attatggatt tttatgaaaaa ctgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280  
 aaaaaaaaaa 2290

&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro



Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580

585

590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser  
 595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile  
 610 615 620

&lt;210&gt; 74

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 74

tcacctggag cctttattgg cc

22

&lt;210&gt; 75

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 75

ataccagcta taaccaggct gcg

23

&lt;210&gt; 76

&lt;211&gt; 52

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 76

caacagtaag tggtttgatg ctcttccaaa tcttagagatt ctgtatgatttg  
 gg

50

52

&lt;210&gt; 77

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 77  
ccatgtgtct cctcctacaa ag 22

<210> 78  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 78  
gggaatagat gtgatctgat tgg 23

<210> 79  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 79  
cacctgttagc aatgcaaatac tcaaggaaat accttagagat ctccctcctg 50

<210> 80  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 80  
agcaaccgcc tgaagctcat cc 22

<210> 81  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 81  
aaggcgccgt gaaagatgta gacg 24

<210> 82

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcaactgg agttggcgaa 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 cccacgcgtc cgcacctcg cccgggctc cgaagcggct cgggggcgcc ctttcggta 60  
 acatcgtagt ccaccccctc cccatccccca gccccccccgattcaggctc gccagcgccc 120  
 agccaggaggccggaga agcgcgatgg gggccccccagc cgcctcgctc ctgctccctgc 180  
 tcctgctgtt cgccctgctgc tggcgccccg gcccccccaaa cctctcccaag gacgacagcc 240  
 agccctggac atctgatgaa acagtggtgg ctggtgccac cgtggtgc aagtggcaag 300  
 tgaaagatca cgaggactca tccctgcaat ggtctaaccctg tgcctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgcccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcagatc acctgctcaa 480  
 tcttcactat gcctgtgcga actgccaagt ccctcgctac tggcttagga attccacaga 540  
 agccatcat cactggttat aaatcttcat tacggaaaa agacacagcc accctaaact 600  
 gtcagtttc tgggagcaag cctgcagccc ggctcacctg gagaagggt gaccaagaac 660  
 tccacggaga accaaccgc accaaccgc atacaggaag atcccaatgg taaaacccctc actgtcagca 720  
 gtcgggtgac attccagggtt acccgggagg atgatggggc ggcacatcg tgcctgtga 780  
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 ctcccgcttg ctccccagcc caccacccctc cctgtacaga atgtctgtt tgggtgcgg 1500  
 ttttactcg gtttggaatg gggagggagg aggggggggg gggggggggg ttgcctctc 1560  
 cccttcgt ggcttctctg catttgggtt attattattt ttgttaacaat cccaaatcaa 1520  
 atctgtatcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1580  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Phe Ala  
 1 5 10 15

Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
 20 25 30

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 85

gcttaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 87		
cctagcacag tgacgaggga cttggc		26
<210> 88		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 88		
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc		50
<210> 89		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 89		
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt		50
<210> 90		
<211> 2755		
<212> DNA		
<213> Homo sapiens		
<400> 90		
gggggttagg gaggaaggaa tccaccccca cccccccaaa ccctttctt ctcccttcct 60		
ggcttcggac attggagcac taaatgaact tgaatttgtt ctgtggcgag caggatggc 120		
gtgttactt tgtatgaga tcggggatga attgctcgct taaaaaatgc tgcttggat 180		
tctgttgctg gagacgtctc ttgttttg: cgctggaaac gttacagggg acgtttgcaa 240		
agagaagata tggccctgca atgagataga aggggaccta caacgttagact gtaaaaaaaa 300		
gggcttcaca agtctgcagc gttcactgc cccgacttcc cagttttacc atttatttct 360		
gcatggcaat tccctcactc gactttccc taatgagttc gctaactttt ataatgcgg 420		
tagttgcac atggaaaaca atggcttgca tggaaatcggtt cggggggctt ttctgggct 480		
gcagctggtg aaaaggctgc acatcaacaa caacaagatc aagtctttc gaaagcagac 540		
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catcagcacc ctacctgcca acgtgttcca gtatgtgccc atcaccacc tcgaccccg 720		
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cagactgcag ggtaaaagacc tcaatgaaac caccgaacag gacttgcgtt ctttggaaaa 960		
ccgagtggtat tctagctcc cggcgcccc tggccaaagaa gagaccttgc ctccctggacc 1020		
cctgccaact ctttcaaga caaatggca agaggatcat gccacaccag ggtctgctcc 1080		

aaacggaggt acaaagatcc caggcaactg gcagatcaa atcagaccca cagcagcgat 1140  
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 caggtggcta tacatggata gcaattacct ggacacgctg tccgggaga aattcgcggg 1500  
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 ctcgcccacg ttaacttcgc acagaaaaa cagcactggg ttggcggaga ccgggacgc 1980  
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 agtgtatgac tgtggcttc actcgcttc agactaagac cccaacccca ataggggagg 2280  
 gcagaggaa ggcgatacat cttccccac cgcaggcacc ccggggctg gaggggctg 2340  
 tacccaaatc cccgcgcct cagcctggat gggcataagt agataaataa ctgtgagctc 2400  
 gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460  
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 atatctattnn tccccctgtg gattagcccc gtgatgctc cctgttggtc acgcaggat 2700  
 gggcagttgc acgaaggcat gaatgtattg taaataagta actttgactt ctgac 2755

&lt;210&gt; 91

&lt;211&gt; 696

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 91

Met	Leu	Leu	Trp	Ile	Leu	Leu	Glu	Thr	Ser	Leu	Cys	Phe	Ala	Ala
1														
													15	

Gly	Asn	Val	Thr	Gly	Asp	Val	Cys	Lys	Glu	Lys	Ile	Cys	Ser	Cys	Asn
													20	30	

Glu	Ile	Glu	Gly	Asp	Leu	His	Val	Asp	Cys	Glu	Lys	Lys	Gly	Phe	Thr
													35	45	

Ser	Leu	Gln	Arg	Phe	Thr	Ala	Pro	Thr	Ser	Gln	Phe	Tyr	His	Leu	Phe
													50	60	

Leu	His	Gly	Asn	Ser	Leu	Thr	Arg	Leu	Phe	Pro	Asn	Glu	Phe	Ala	Asn
													65	75	80

Phe	Tyr	Asn	Ala	Val	Ser	Leu	His	Met	Glu	Asn	Asn	Gly	Leu	His	Glu
													85	90	95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190

Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205

Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220

Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240

Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270

Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285

Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300

Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320

Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335

Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350

Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365

Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660

665

670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
 675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
 690 695

&lt;210&gt; 92

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 92

gttggatctg ggcaacaata ac

22

&lt;210&gt; 93

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 93

attgttgtgc aggctgagtt taag

24

&lt;210&gt; 94

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 94

ggtggtata catggatagc aattacctgg acacgtgtc ccggg

45

&lt;210&gt; 95

&lt;211&gt; 2226

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

agtgcactgc gtccccctgtta cccggcgcca gctgtgttcc tgaccccaga ataactcagg 60  
 gtcgcacccgg gcctggcagc gctccgcaca catttcctgt cgccggctaa gggaaactgt 120  
 tggccgctgg gccccgggggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

gaggggaagg gaggggaaac cgggttgggg aagccatcg tagagggcgg tgaccgcgt 240  
 ccagacacag ctctgcttc tegagcggga cagatccaag ttggggacag ctctgcgtgc 300  
 ggggccttag agaatgagc cggcgttcgc cctgtgcctc ctctggcagg cgctctggcc 360  
 cgggcccggc ggccggcaac accccactgc egaccgtgt ggctgtcggg cctcggggc 420  
 ctgctacagc ctgcaccacg ctaccatgaa gcccggcggc gccgaggagg cctgcattct 480  
 gcgaggtggg gcgctcagca cctgtcgtgc gggccgcggag ctgcgcgtcg tgctgcgtc 540  
 cctgcggca ggcccaggc cccggagggg ctccaaagac ctgtgttct gggtcgcact 600  
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 ctcctgcacc gcgcggagat ggcggtaact ccaggccacc ggtggggctcg agccccgcagg 780  
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 ggagaatttg gagaagtgtat tgaactttc aagacattgg aaacaaatag aacacaatat 2100  
 aatttacatt aaaaaataat ttctacaaa atggaaagga aatgttctat gttgttcagg 2160  
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 gttgtat 2226

<210> 96  
 <211> 490  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
 Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
 1 5 10 15

Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80

Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln



<210> 99  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 99  
acagagcaga gggtgccattg 20

<210> 100  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 100  
tcagggacaa gtgggtctc tccc 24

<210> 101  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 101  
tcagggagg agtgtgcagt tctg 24

<210> 102  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 102  
acagctcccg atctcagtta cttgcattgc ggacgaaatc ggcgctcgct 50

<210> 103  
<211> 2026  
<212> DNA  
<213> Homo sapiens

<400> 103  
cggaacgcgtg ggattcagca gtggccctgtg gtcgtccagag cagctccctca ggggaaacta 60  
agcgctcgagt cagacggcac cataatcgcc tttaaaaagtgt cctccgcct gccggccgcg 120  
tatccccccgg ctaccctgggc cgccccggcg cggtgccgcgt gtgagaggga ggcggccggc 180  
agccgagcgc cgggtgtgagc cagcgctgtc gccagtgtga gcccgggtgt gagcgccgtg 240  
ggtgcggagg ggcgtgtgtg cggcgccgcg cggcgccggc tgcaaaccccc gagcgctctac 300  
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cagctctcgc ggcagcagtc cccagagaga cctgtttca catgtggtgg cattcttaact 420  
ggagagctg gatttattgg cagtgaaggt tttcctggag tgtaccctcc aaatagcaa 480  
tgtacttggaa aaatcacagt tcccgaagga aaagtagtgc ttctcaattt ccgattcata 540  
gacctcgaga gtgacaacact gtgcgcgtat gactttgtgg atgtgtacaa tggccatgcc 600  
aatggccagc gcattggccg cttctgtggc acttccgcg ctggagccct tgggtccagt 660  
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gcccattttcc cggctgtgt accaaacgaa agaggggatc agtattgtgg aggactcctt 780  
gacagacctt cccggctttttaaaaacccca aactggccag accgggatta ccctgcagaa 840  
gtcaacttggt gttggcacat tggtagccca aagaatcagg ttatagaatt aaagtttgag 900  
aagtttgatg tggagcggaga taactactgc cgatatgatt atgtggctgt gtttaatggc 960  
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atgtgtctg agagaaatga acttcttatt cagttttat cagacttaag tttactgca 1080  
gatgggttta ttggtcacta catattcagg ccaaaaaaaac tgcctacaac tacagaacag 1140  
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caaaaagtgtt gacggacggg gactctggag ggcaattatt gttcaagtga ctttgttatta 1260  
gcccggactg ttatcacaac catcaactgc gatgggagtt tgcacgcac agtctcgatc 1320  
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ctaaaagtgtt caagcgttgc cagcttggaa gctgtttattt atacatctt gtaaaaaggat 1860  
attttagaat tggatgtgtt gaaatgtca aaaaaagatt ttagaaatgtc aatattttata 1920  
gtgttatttgc tttcaccttc aaccccttgc cctgaggtgt tacaatcttgc tcttgcgtt 1980  
tctaaatcaa tqcttaataa aatattttt aaaaqaaaaaaa aaaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala  
 1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr  
20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly  
35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr  
 50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Phe Pro Val Thr Thr  
 275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala



<213> Homo sapiens

<400> 108

ggacgcgtg ggccggacgcg tggggggccc acggcgcccc cgggctgggg cggtcggttc 60  
ttccttctcc gtggcctacg agggtccccca gcctggtaa agatggcccc atggccccccg 120  
aagggcctag tcccagctgt gctctggggc cttagcctct tcctcaacct cccaggac 180  
atctggctcc agccctctcc acctccccag ttctctcccc cgcttcagecc ccatccgtgt 240  
catacctgcc ggggactggg tgacagctt aacaaggccc tggagagaac catccggac 300  
aactttggag gtggaaacac tgccctggag gaagagaatt tgccaaata caaagacagt 360  
gagaccgcgc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgcac 420  
cgccctgtgg agtcgagtga ggagctggg gagagctggg gtttcacaa gcagcaggag 480  
gccccggacc tcttccagtg gctgtgtca gattccctga agctctgtc ccccgccaggc 540  
accttcgggc ctcctgcct tccctgtctt gggggaaacag agaggccctg cggtggctac 600  
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660  
tacgggggtg aggccctgtgg ccagtgtggc ctggctact ttgaggcaga acgcaacgccc 720  
agccatctgg tatgttcggc ttgtttggc ccctgtgcct gatgetcagg aectgaggaa 780  
tcaaactgtt tgcaatgcaa gaagggtctgg gcctgcata acctcaagtg ttagacatt 840  
gatgagtggtg gcacagaggg agccaactgt gagagctgacc aattctgcgt gaacactgag 900  
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gcccaggatc ccaggccccgg gcagacaagg ccctggggg aaaaagttagc cctgaagggt 1560  
gataccatga gcttttccacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620  
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acaggggtgg ggcacatcaca gtcctctt gcaagctgca tgctggcagt ttctgttctg 1740  
tgttcaccac atccccacac cccattgcca ttatattt catctcaggaa aataaaagaaa 1800  
qqtcttggaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly  
1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser  
20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr  
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile  
       50                 55                         60

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Glu Ala Cys  
 180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
 405 410 415

Ile Lys Gly Arg  
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcgac ac

22

<210> 113

&lt;211&gt; 1616

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (1461)

&lt;223&gt; a, t, c or g

&lt;400&gt; 113

tgagaccctc ctgcagcctt ctcaggac agcccactc tgccctttgc tcctccaggg 60  
 cagcaccatg cagccccgt ggcactctgg gtgttgcccc tggccagccc 120  
 cggggccgcc ctgacccggg agcagctcct gggcagctg ctgcggcagc tgcaagtc当地 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcatcccc cccacgttag 240  
 ggcccagtac gtggccctgc tgcaagcag ccacggggac cgctcccgcc gaaagagggt 300  
 cagccagage ttccgagagg tgccggcag gttccctggcg ttggaggcca gcacacacct 360  
 gtgggtgttc ggcattggagc agcggctgac gcccaacagc gagctgggtc aggccgtgt 420  
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 ggcgcaggcc cggggccccc tgaccgtcga gtggctgcgc gtccgcgac acggctccaa 540  
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 cgacgtgacc gaggccgtga acttctggca gcagctgac cgccccggc agccgctgt 660  
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 ggtccgctt gcctcgagg gggccgcagg cggcgttggg gageccccagg tggagctgca 780  
 cacccctggac cttggggact atggagctca gggcactgt gaccctgaag caccaatgac 840  
 cgagggcacc cgctgctgcc gecaggagat gtacattgac ctgcagggga tgaagtggc 900  
 cgagaactgg gtgctggagc ccccggtt cttcaagtg gccgttctg gggcctcgac agtgcattgc 960  
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 ctccggagact gactcgctgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080  
 ccagggtggc agcctgccc acatgagggt gcagaagtgc agtgcattgc cggatggc 1140  
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 gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgtgactg aactgctgat 1260  
 ggacaaatgc tctgtgtct ctgtgagcc ctgaatttgcc ttcccttgac aagttacctc 1320  
 acctaatttt tgcttctcag gaatgagaat cttggccac tggagagccc ttgctcagg 1380  
 ttctcttattc ttatttca ctgcactata ttctaaagcac ttacatgtgg agatactgta 1440  
 acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggt 1500  
 aaagtctcc accaccactc tggacctaag acctgggtt aagtgtgggt tgtgcattccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

&lt;210&gt; 114

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 114

Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala

1

5

10

15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu

20

25

30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met

35

40

45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115

aggactgcca taacttgccc g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117

tgttgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtccctt cggcggtgtgt tggtcaagtgcctgatcgcatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcataat tggcgatccct gttgtgtcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcaaat tcctgagaat 180

aatcctgtga agtgtcctg tgccactactcg ggcttttctt ctccccgtgt ggagtggaaag 240  
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300  
gaggaccggg tgacccctt gccaactgggt atcaccttca agtccgtgac acgggaagac 360  
actgggacat acacttgtat ggtctctgag gaaggccggca acagctatgg ggaggtcaag 420  
gtcaagctca tcgtgcttgc gcctccatcc aagcctacag ttaacatccc ctctctgcc 480  
accattgggaa accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540  
tacacctggt tcaaagatgg gatagtgtat cctacgaatc caaaaagcac ccgtgccttc 600  
agcaacttcc cctatgttctt gaatccacaca acaggagagc tggctttga tccccgtca 660  
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatggac acccatgact 720  
tcaaatgtctg tgccatggaa agctgtggag cggaaatgtgg gggtcatcgt ggcagccgtc 780  
cttgaaccc tgattcttcc gggaaatcttgc tttttggca tctggttgc ctatagccga 840  
ggccactttg acagaacaaa gaaaggact tcgagaatgg aggtgatttca cagccagcct 900  
agtgcggaa gtgaaggaga attcaaacag acctcgatcat tcctgggtgt agcctggtcg 960  
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tctagagccg gaatttagagg cttagagccg tggaaatgggt gtttgggtat gacactgggg 1440  
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cagaggctga ggcaggccgaa tcacctggagg tcgggagttc gggatcagcc tgaccaacat 1740  
ggagaaaaaccctt tactggaaat acaaaggtag ccaggcatgg tggctgtatgc ctgttagtccc 1800  
agctgctcag gagctggca acaagagca aactccagct caaaaaaaaaaaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
       50                 55                         60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 120

tgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 121  
tgatcgcgat ggggacaaag gcgcaagctc gagagggaaac tgggtgtgcct 50

<210> 122  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 122  
acacctggtt caaagatggg 20

<210> 123  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 123  
taggaagagt tgctgaaggc acgg 24

<210> 124  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 124  
ttgccttact cagggtgtac 20

<210> 125  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 125  
 aactcagcagt ggttagaaaag 20

<210> 126  
<211> 1210  
<212> DNA  
<213> Homo sapiens

<400> 126  
 cagcgcgtgg ccggcgccgc tgggggaca gcatgagcgg cggttggatg ggcgcagggtt 60  
 gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcgcc ctcggactag 120  
 gcctggaggc cgccgcgagc ccgcgttcca ccccgcaccc tgcccgaggcc gcaggcccc 180  
 gtcaggctc gtgcccaccc accaagtcc agtgcgcac cagtggctta tgcgtgcccc 240  
 tcacctggcg ctgcgacagg gacttggact gtagcgtgg cagcgtatgg gaggagtgc 300  
 ggattgagcc atgtaccagg aaaggcaat gcccacccgc ccttgcgcctc ccctggccct 360  
 gcacccggcgt cagtgaactgc tctggggaa ctgacaagaa actgcgcac tgcagccgc 420  
 tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
 ggcgcgtgcga cggccaccca gactgtcccg actccagcga cgagctcgcc tgtggAACCA 540  
 atagagatctt cccggaagg gatgccacaa ccatggggcc ccttgcgtgacc ctggagatgt 600  
 tcacctctct caggaatgcc acaaccatgg ggcccccgt gaccctggag agtgtccct 660  
 ctgtcgaa tgccacatcc tcctctgcgg gagaccagtc tgaagccca actgcctatg 720  
 gggttattgc agctgctgcg gtgttcgtg caagcctggt caccgcacc ctcctccctt 780  
 tgcgtggct ccgcgcctcc gagcgcctcc gcccactggg gttactgggtg gccatgaagg 840  
 agtccctgtc gctgtcagaa cagaagaccc cgcgcctcg aggacaagca cttgcacca 900  
 ccgtcactca gcccggcg tagccggaca ggaggagagc agtgcgcgg atgggtaccc 960  
 gggcacacca gcccctcagag acctgagttc ttctggccac gtggaaacctc gaaccggcgc 1020  
 tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080  
 agctaggatg gggAACCTGC cacagccaga actgaggggc tggccccagg cagctcccg 1140  
 gggtagaac ggcctgtgc ttaagacact ccctgcgtcc ccgtctgagg gtggcgattt 1200  
 aagttgttc 1210

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
 Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
 1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
 20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
 35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
 50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
 65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
 85 90 95

Lys Gly Gln Cys Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
 100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
 145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
 165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
 195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala  
 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln  
 245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
 cccacgcgtc cggtctcgct cgctcgcgca gcggcgccag cagaggctcg gcacagatgc 60  
 gggtagact ggccggggga ggaggcgag gagggaaagga agctgcgtgc atgagacc 120  
 cagactcttg caagctggat gcctctgtg gatgaaaat gtatcatgaa atgaacccg 180  
 gcaatggaga tggatttcta gagcagcagc agcagoagca gcaacccatcg tccccccaga 240  
 gactcttggc cgtgatcctg tggttcagc tggcgctgtg ctccggccct gcacagctca 300  
 cggccgggtt cgatgacatt caagtgtgtg ctgaccccg cattcccgag aatggctca 360  
 ggaccccccag cggagggggtt ttctttaag gctctgtac ccgatttcac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtataat tccatctgtg tgcaagaaga ttggcgatc cctcaatcg 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaattt atcacttgc 600  
 atgaaggatt caagatccgg taccggacc tacacaatat ggtttcatta tgtcgatg 660  
 atgaaacgtg gaataatctg cccatctgtc aaggctcgct gagacccctta gctcttcta 720  
 atgctatgt aaacatctt gagctccaga ctccttccc gttggggact gtgatctct 780  
 atcgctgctt tcccgattt aaaccttgcgtt ggtctcgatc tcttgatgc ttacaaaacc 840  
 ttatctggc gtccagccca ccccggtgcc ttgctctgaa agcccaagtc tgcactac 900  
 ctccaatggt gagtcacgga gatttcgtct gccaccccgcc gcttgcgtgag cgctacaacc 960  
 acgaaactgt ggtggagtt tactgcgtc ctggctacag ctcaccaggc gactacaagt 1020  
 acatcacctg ccagtatgga gatggtttc cttcttatca agtctactgc atcaaatcg 1080  
 agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtgaaagatt gtggcgatc 1140

cggcaaccag tggctgtctg gtggctgc tcgtcatcct gcccaggatg ttccagacca 1200  
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 ttgtggtgt agacggcgtg cccgtcatgc tcccgctcta tgacgaagct gtgagtgccg 1320  
 gcttgagtgc cttagggccc gggtacatgg cctctgtggg ccagggctgc cccttacccg 1380  
 tggacgacca gagcccccca gcataccccc gctcaggggc cacggacaca ggcccagggg 1440  
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 ctcccagggtg ccaagagagc acccaccctg cttcggacaa cctgtacata attgccagca 1560  
 cggcagagaga ggtggcatcc accagcccag gcatccatca tgcccactgg gtgtgttcc 1620  
 taagaaaactg attgattaaa aaatttccc aagtgtcctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt ccttccttc tcttgggttt agacaaatgt aaacaaagct 1740  
 ctgatcctta aaattgctat gctgatagag tggtagggc tggaaagctt atcaagtcct 1800  
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1															15

Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
					5									30

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
								35						45	

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
					50			55						60	

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
					65				70					80	

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
					85				90					95	

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
						100			105					110	

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
						115			120					125	

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
						130		135					140		

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
							145						155	160	

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
						165			170					175	

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133  
 attcctatc gctgcttcc cg 23

<210> 134  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134  
 agccaggatc gcagtaaaac tcc 23

<210> 135  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135  
 atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct 50

<210> 136  
 <211> 1815  
 <212> DNA  
 <213> Homo sapiens

<400> 136  
 cccacgcgtc cgctccgcgc cctccccccc gcctccgtg cggccgtcg gtggccaga 60  
 gatgctgctg ccgcgggtgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120  
 ccgttagcgcc cgagtgtcgg ggggegcacc cgagtcgggc catgaggccc ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggctgctg ggcgcgcacg ggtcgcctgc 240  
 tgagtgcctc ggatttggac ctcaagaggag ggcagccagt ctgcgcgggga gggacacaga 300

ggccttggta taaagtccatt tactttccatg atacttctcg aagactgaac tttgaggaag 360  
ccaaagaaggc ctgcaggagg gatggaggcc agcttagtcag catcgagtct gaagatgaac 420  
agaaaactgat agaaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480  
ggctcaggag ggttggggag aaacaaagca atagcacagc ctggcaggac ctttatgctt 540  
ggactgatgg cagcatatca caatttagga actggatgtt ggatgagccg tcctgcggca 600  
ggggggctg cgtggtcatg taccatcage catcgccacc cgctggcattc ggaggcccct 660  
acatgttcca gtggaatgtat gaccggtgca acatgaagaa caatttcatt tgcaaataatt 720  
ctgatgagaa accagcagtt ccttcttagag aagctgaagg tgagggaaaca gagctgacaa 780  
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaaagta 840  
gagaagctgc cttgaatctg gcctacatcc taatccccag cattccctt ctccctctcc 900  
tttgtggcac cacagttgtt tgggggttt ggatctgttag aaaaagaaaa cgggagcagc 960  
cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag gggaaacagcc 1020  
cgacccatgg ggttacaat gtcataagaa aacaaagcga agctgactta gtttggggcc 1080  
ggccagacct gaagaatatt tcattccggat tgggggttt ggatctgttag aaaaagaaaa cccgatgaca 1140  
tgttgggtga ctatgacaac atggctgtga accccatcaga aagtgggttt gtgactctgg 1200  
tgagcgttgg ggttggattt gtgaccaatg acatttatga gtttccccc gaccaatagg 1260  
ggaggagtaa gggttggat tgggggtttt atgaaaatata tggttatttag gacatataaa 1320  
aaactgaaac tgacaacaat gggaaaagaaaa tgataagcaa aatccttta ttttctataa 1380  
ggaaaataca cagaagggtct atgaacaagc tttagatcagg tcctgtggat gagcatgtgg 1440  
tccccacgac ctccctgttgg accccacgt tttggctgttgc tccttcttcc cagccagtc 1500  
tccagctcga ccttatgaga aggtacccgtt cccagggtctg gcacatagta gagtctcaat 1560  
aaatgtcact tgggttgggtt tatctaactt ttaagggaca gagcttacc tggcagtgt 1620  
aaagatgggc tggggagctt gggaaaaccac ctctgttttc cttgtctat acagcagcac 1680  
atattatcat acagacagaa aatccagaat cttttcaaaag cccacatatg gtggcacaagg 1740  
ttggcctgtg catcgccaaat tctcatatct gttttttca aagaataaaaa tcaaataaaag 1800  
agcaggaaaa aaaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met	Arg	Pro	Gly	Thr	Ala	Leu	Gln	Ala	Val	Leu	Leu	Ala	Val	Leu	Leu
1					5				10					15	

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
                  85                   90                   95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 140  
 cagtccaagc ataaaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgccg acttgggggc gcccgcgtgag ccccgccgcgc cgcagaagac 120  
 ttgtgtttgc ctccctgcagc ctcaaccggg agggcagcga gggccttacca ccatgatcac 180  
 tggtgtgttc agcatgcgtc tggacccccc agtggggcgtc ctgacacccgc tggcgtaactg 240  
 cctgcaccag cggcggttgg ccctggccga gctgcaggag gccgatggcc agtgtccgggt 300  
 cgaccgcagc ctgtctgaagt taaaaatggt gcaggtcggt tttcgacacg gggctcgag 360  
 tcctctcaag cgcgtccccgc tggaggagca ggttagagtgg aaccccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctgggtggc cggaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctggca 540  
 gctgaccaag gtggggcatgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attcccttgc tttcaccaac cttcaacccca caggaggtct ttattcgttc 660  
 cactaacatt tttcggaatc tggagtccac ccgttggc ctggctggc tttccagtg 720

tcagaaaagaa ggaccatca tcatccacac tcatgaagca gattcagaag tcttgatcc 780  
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840  
 ttacagcca ggaatctcg aggattgaa aaaggtgaag gacaggatgg gcattgacag 900  
 tagtataaa gtggacttct tcatcctcct ggacaacgtg gtcggcggc aggcacacaa 960  
 cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020  
 cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggccc 1080  
 attccctccac atcctagaga gcaacctgct gaaagccatg gactctgcc 1140  
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200  
 gaccctgggg attttggacc acaaatggcc accgttgct gttgacactga ccatgaaact 1260  
 ttaccagcac ctggaatcta aggagtggtt tgtcagatc tattaccacg ggaaggagca 1320  
 ggtgccgaga ggtgccctg atggctctg cccgctggac atgttcttga atgcatgtc 1380  
 agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440  
 agttggaaat gaagagtaac tgatttataa aagcaggatg tttgatttt aaaataaaat 1500  
 gccttatac aatg 1514

&lt;210&gt; 142

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

Met	Ile	Thr	Gly	Val	Phe	Ser	Met	Arg	Leu	Trp	Thr	Pro	Val	Gly	Val
1															15

Leu	Thr	Ser	Leu	Ala	Tyr	Cys	Leu	His	Gln	Arg	Arg	Val	Ala	Leu	Ala
			20						25				30		

Glu	Leu	Gln	Glu	Ala	Asp	Gly	Gln	Cys	Pro	Val	Asp	Arg	Ser	Leu	Leu
									35				40		45

Lys	Leu	Lys	Met	Val	Gln	Val	Val	Phe	Arg	His	Gly	Ala	Arg	Ser	Pro
								50					55		60

Leu	Lys	Pro	Leu	Pro	Leu	Glu	Glu	Gln	Val	Glu	Trp	Asn	Pro	Gln	Leu	
									65					70	75	80

Leu	Glu	Val	Pro	Pro	Gln	Thr	Gln	Phe	Asp	Tyr	Thr	Val	Thr	Asn	Leu
								85					90		95

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu
									100				105		110

Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly
									115				120		125

Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val
									130				135		140

Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe	
									145				150		155	160

Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu
									165				170		175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425  
 <210> 143  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 143  
 ccaactacca aagctgctgg agcc 24

<210> 144  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 144  
 gcagcttat taccacggga agga 24

<210> 145  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 145  
 tccttcccggt ggtaatagag ctgc 24

<210> 146  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 146  
 ggcagagaac cagaggccgg aggagactgc ctcttacag ccagg 45

<210> 147  
 <211> 1686  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 ctctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
 cttaaaatttc agctcatcac cttcacctgc cttggcatg gctctgctat tctccttgat 120  
 cttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtgg 180



Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240  
 Pro Phe Asp Leu Arg Leu Val Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 149		
ttcagctcat cacccatcacc tgcc		24
<210> 150		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 150		
gggtcataca aaataccact aggg		24
<210> 151		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 151		
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt		50
<210> 152		
<211> 1427		
<212> DNA		
<213> Homo sapiens		
<400> 152		
actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgaccccg 60		
accacacgcgt ccgcggacgc gtggggcgac gcgtggcccg gctaccagga agagtctgcc 120		
gaaggtgaag gccatggact tcacacccctc cacagccatc ctgcggccctgc tggctggctg 180		
cctggggcgtc ttccggccctct tccggctgct gcagtgggtg cgccggaaagg cctacccctgc 240		
gaatgtgtg gtggtgatca caggcgccac ctcaggccgt ggccaaagaat gtgcaaaagt 300		
cttctatgt gcgggtgtcta aactgtgtct ctgtggccgg aatgggtgggg ccctagaaga 360		
gctcatcaga gaacttaccg cttctatgc caccaaggtg cagacacaca agccttactt 420		
ggtgacccctc gacccacacag actctggggc catagttgca gcacgcgtg agatcctgca 480		
gtgttttggc tatgtcgaca tacttgtcaa caatgtggg atcagctacc gtggtaccat 540		
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccgagt 600		
tgctctaactc aaaggactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgcc 660		
catcagcagc atccaggccca agatgagcat tcctttcga tcagcatatg cagccctccaa 720		
gcacgcaacc caggcttct ttgactgtct gcgtggccgag atggAACAGT atgaaattga 780		
ggtgaccgtc atcagccccg gctacatcca caccaacccctc tctgttaaatgg ccatcacccgc 840		
ggatggatct aggtatggag ttatggacac caccacagcc caggccgaa gcccctgtgga 900		
ggtgcccgag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctgctgaa 960		
cttactgcct tccttgctg tttatcttcg aactctggct cctgggctct tcttcagcc 1020		
catggccctcc agggccagaa aagagccgaa atccaagaac tccttagtact ctgaccagcc 1080		

agggccaggc cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcac 1140  
 ttgtgagac tttaatggag atttgtctca caagtggaa agactgaaga aacacatctc 1200  
 gtgcagatct gctggcagag gacaatcaa aacgacaaca agcttcttcc cagggtgagg 1260  
 gaaaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320  
 tctcaaacag taaaaaaaaaaa aaaaaaggjc ggccgcact ctagactcgaa cctgcagaag 1380  
 cttggccgcc atggcccaac ttgttattg cagttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met	Asp	Phe	Ile	Thr	Ser	Thr	Ala	Ile	Leu	Pro	Leu	Leu	Phe	Gly	Cys
1															15

Leu	Gly	Val	Phe	Gly	Leu	Phe	Arg	Leu	Leu	Gln	Trp	Val	Arg	Gly	Lys
															30

Ala	Tyr	Leu	Arg	Asn	Ala	Val	Val	Val	Ile	Thr	Gly	Ala	Thr	Ser	Gly
35															45

Leu	Gly	Lys	Glu	Cys	Ala	Lys	Val	Phe	Tyr	Ala	Ala	Gly	Ala	Lys	Leu
50															60

Val	Leu	Cys	Gly	Arg	Asn	Gly	Gly	Ala	Leu	Glu	Glu	Leu	Ile	Arg	Glu
65															80

Leu	Thr	Ala	Ser	His	Ala	Thr	Lys	Val	Gln	Thr	His	Lys	Pro	Tyr	Leu
85															95

Val	Thr	Phe	Asp	Leu	Thr	Asp	Ser	Gly	Ala	Ile	Val	Ala	Ala	Ala	
100															110

Glu	Ile	Leu	Gln	Cys	Phe	Gly	Tyr	Val	Asp	Ile	Leu	Val	Asn	Asn	Ala
115															125

Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Ile	Met	Asp	Thr	Thr	Val	Asp	Val	Asp
130															140

Lys	Arg	Val	Met	Glu	Thr	Asn	Tyr	Phe	Gly	Pro	Val	Ala	Leu	Thr	Lys
145															160

Ala	Leu	Leu	Pro	Ser	Met	Ile	Lys	Arg	Arg	Gln	Gly	His	Ile	Val	Ala
165															175

Ile	Ser	Ser	Ile	Gln	Gly	Lys	Met	Ser	Ile	Pro	Phe	Arg	Ser	Ala	Tyr
180															190

Ala	Ala	Ser	Lys	His	Ala	Thr	Gln	Ala	Phe	Phe	Asp	Cys	Leu	Arg	Ala
195															205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile	Thr Ala Asp Gly Ser Arg	
225	230	240
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val		
260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
290	295	300
Arg Lys Ser Lys Asn Ser		
305	310	

&lt;310&gt; 154

&lt;311&gt; 24

&lt;312&gt; DNA

&lt;313&gt; Artificial Sequence

&lt;320&gt;

<323> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 154

gggtqctaaac tggtgctctg tggc

24

&lt;310&gt; 155

&lt;311&gt; 20

&lt;312&gt; DNA

&lt;313&gt; Artificial Sequence

&lt;320&gt;

<323> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 155

caggggcaaga tgagcattcc

20

&lt;310&gt; 156

&lt;311&gt; 24

&lt;312&gt; DNA

&lt;313&gt; Artificial Sequence

&lt;320&gt;

<323> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156  
 tcatactgtt ccatctcgac acgc 24  
  
 <210> 157  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 157  
 aatgggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50  
  
 <210> 158  
 <211> 1771  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 158  
 cccacgcgtc cgctgggttt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
 aaaaaaaaaa acacacccaa cgctcgacg cacaaaaggg atgaaatttc ttctggacat 120  
 cctcctgttt ctcccggtac tgatcgctg ctccttagag tccttcgtga agcttttat 180  
 tcctaagagg agaaaatcg tcaccggcga aatcgctg attacaggag ctggcatgg 240  
 aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
 tataaataag catggactgg agggaaacago tgccaaatgc aagggaactgg gtgccaagg 360  
 tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaagg 420  
 gaaggcagaa attggagatg ttagtatttt agtaaataat gctggtagtgc tctatacatc 480  
 agatttggtt gctacacaag atcctcagat tgaaaagact ttgaagtta atgtacttgc 540  
 acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
 tgtcaactgtg gcttcggcag ctggacatgt ctgcgtcccc ttcttactgg cttactgttc 660  
 aagcaagttt gctqctqttt gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
 aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gttcatcaa 780  
 aaatccaagt acaagttgg gacccactct ggaacctgag gaagtggtaa acaggctgat 840  
 gcatgggatt ctgactgagc agaagatgat ttttatttcca tcttctataa ctttttaac 900  
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 taagtttgc gcaatttttgc gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020  
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 ctctgtttt ttcttaattt cccatttttgc tcaatatcat ttttggggct ttggcagtct 1140  
 tcatttacta ccacttgc ttttagccaaa agctgattac atatgatata aacagagaaa 1200  
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 taatttccaa gattatttgt ggctcacctg aaggcttgc aaaatttgc ccataaccgt 1320  
 ttattnaca tatatttttgc ttttgatttgc cacttaatttgc ttttgcataatttgc ttttgcatttttgc 1380  
 ttctgttct acataaaatc agaaaacttca agctcttca ataaaatgaa ggactatatc 1440  
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 gccactctgt ttccctgagag atacctcaca ttccaaatgcc aaacatttgc gcacaggaa 1560  
 gcttagaggtg gatacacgtg ttgcaagtataaaaggatca ctgggatttgc aggagaatttgc 1620  
 agagaatgtt cccacaaatgc gcagcaataa taaatggatc acacttaaaa aaaaaaaaaaaa 1680  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1771

<210> 159

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
1															15

Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
															30
20								25							

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
															45
35							40								

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
															50
								55			60				

Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
															65
								70		75					

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
															85
								90					95		

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
															100
								105							110

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
															115
								120				125			

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
															130
								135		140					

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
															145
								150		155			160		

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
															165
								170				175			

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
															180
								185				190			

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
															195
								200		205					

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
															210
								215		220					

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
															225
								230		235		240			

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
															245
									250			255			

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 160

ggtaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 162

gttgtgttag tctatacatac agatttgttt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

ccccacgcgtc cgccggacgcg tgggtcgact agttctagat cgcgagcgcc cggccgcggc 60  
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggtg 120

attgttcgc tggcctgtt gatgcctggc ccctgtatg ggctgtttcg ctccctatac 180  
 agaagtgtt ccatgccacc taagggagac tcaggacagc cattatttct cacccttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300  
 ctgaacatga agagttatgc cggttcctc accgtaaata agacttacaa cagcaacetc 360  
 ttcttcgtt ctgtccacgc tcagatacag ccagaagatg cccagtagt tetctggcta 420  
 cagggtggc cgggagggttc atccatgtt ggactcttg tggAACATGG gcttatgtt 480  
 gtcacaagta acatgaccc gcgtgacaga gacttccct ggaccacaac gctctccatg 540  
 ctttacattg acaatccagt gggcacaggc ttcaGTTA ctgtatgatac ccacggat 600  
 gcagtcaatg aggacgtgt agcacggat ttatacagtg cactaattca gttttccag 660  
 atatttcctg aatataaaaa taatgactt tatgtcaactg gggagtctta tgcagggaaa 720  
 tatgtccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
 aacctgaacg gaattgtat tggagatgga tattctgtatc ccaaatcaat tatagggggc 840  
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 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggttga ggccttgaa 960  
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 tttaatgatg gaactatagt tggaaatgtac ttgcgagaag atacagtaca gtcagtaag 1200  
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 caggaataca agaaggcaga aaaaaaagt tggagatct ttaaatctga cagtgaagtg 1380  
 gctggtaa tccggcaagc gggtgactt catcaggtaa ttattcgagg tggaggacat 1440  
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 tcatatctgc aagatTTTTC tcataataa aaattatcct tggaaacaagt gagctttgt 1680  
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&lt;210&gt; 164

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 164

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1															15

Pro	Gly	Pro	Cys	Asp	Gly	Leu	Phe	Arg	Ser	Leu	Tyr	Arg	Ser	Val	Ser
															30
20															

Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
															45
35															

Ile	Glu	Ala	Gly	Lys	Ile	Gln	Lys	Gly	Arg	Glu	Leu	Ser	Leu	Val	Gly
															60
50															

Pro	Phe	Pro	Gly	Leu	Asn	Met	Lys	Ser	Tyr	Ala	Gly	Phe	Leu	Thr	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln			
85		90	95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100		105	110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115		120	125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130	135	140	
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145	150	155	160
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165		170	175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180		185	190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195		200	205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210	215	220	
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225	230	235	240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245		250	255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260		265	270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275		280	285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290	295	300	
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305	310	315	320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325		330	335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340		345	350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
                  370                   375                   380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

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<210> 165
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165  
ttccatgccat cctaaggag actc

24

```
<210> 166
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166  
tggatgaggt gtgcaatggc tggc

24

```
<210> 167  
<211> 24  
<212> DNA  
<213> Artificial Sequence
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```

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 167
agctctcaga ggctggtcat aggg                                24

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gtttcctcac      50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
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atttttccct ttcttaacaa gttctaacag ctgttctaac agctagtgt caggggttct 120
tcttgcttggaa gaagaaaaggg ctgagggcag agcagggcac tctcaacttag ggtgaccagc 180
tccttgcctc tctgtggata acagagcatg agaaaagtgaa gagatgcagc ggagttaggt 240
gatggaaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gaggcgttga 300
cctggagagc ctgggggagg gcctgcctaa caagcttta aaaaacagga gcgacttcca 360
ctgggcttggg ataagacgtg ccggtaggat agggaaagact gggttagtc ctaatatcaa 420
attgactggc tgggtgaact tcaacagctt ttaacctct ctgggagatg aaaacgttgg 480
cttaaggggc cagaaataga gatgcttggaaaataaaaaat ttaaaaaaaaa gcaagtattt 540
tatagcataa aggctagaga cccaaataga taacaggatt ccctgaacat tcctaaagg 600
gagaaagtat gtaaaaaaaaa gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
accaggatgg ggaccctggg tcagggcagc ctctttgctc ctccccggaaa ttattttgg 720
tctgaccact ctgccttggg ttttgcagaa tcatgtgagg gccaaccggg gaagggtggag 780
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ctcatcaaga tcccttcaga caccctggcc ctggtctccc actttgacat ttctacatc 1560
taaggcttg ctatgtgggg ctggatgggac tttctactg tccagccgaa gaccctgag 1620
ggtgtggcca tcaactccgc tggagaccc ttctacaccc cacgcacatcg tggctctgc 1680

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aaggatgacc ccaagttcca ctcatacgtg tccctgcct tcggctgcac ccggggcg 1740  
 gtggaaatacc gcctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800  
 gccttaata tcaccagcca ggacgatgtt ctcttgcca tcttctccaa agggcagaag 1860  
 cagtatcacc acccgccccga tgactctgcc ctgtgtgcct tccttatccg ggccatcaac 1920  
 ttgcagatca aggagcgcct gcagtctgc taccaggcg aggcaacct ggagctcaac 1980  
 tggctgctgg ggaaggacgt ccagtgcacg aaggcgctg tcctccatcga tgataacttc 2040  
 tgtggactgg acatcaacca gcccctggg ggctcaactc cagtgagggg cctgaccctg 2100  
 tacaccacca gcagggacccg catgacccctt gtggccctt acgtttacaa cggctacagc 2160  
 gtggtttttgg tggggactaa gagtggcaag ctgaaaaagg taagagtcta tgagttcaga 2220  
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 agatttaact ataggcaact ttatttctt gggaaacaaa ggtgaaatgg ggaggtaaga 2340  
 aggggttaat ttgtgactt agttcttagc tacttcctcc accatcagt cattgggtat 2400  
 gtaaggaatg caagcgtatt tcaatatttcc caaaacttta agaaaaaaact ttaagaaggt 2460  
 acatctgcaa aagcaaa 2477

&lt;210&gt; 170

&lt;211&gt; 552

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 170

Met	Gly	Thr	Leu	Gly	Gln	Ala	Ser	Leu	Phe	Ala	Pro	Pro	Gly	Asn	Tyr
1														15	

Phe	Trp	Ser	Asp	His	Ser	Ala	Leu	Cys	Phe	Ala	Glu	Ser	Cys	Glu	Gly
														30	
20															

Gln	Pro	Gly	Lys	Val	Glu	Gln	Met	Ser	Thr	His	Arg	Ser	Arg	Leu	Leu
														45	
35															
40															

Thr	Ala	Ala	Pro	Leu	Ser	Met	Glu	Gln	Arg	Gln	Pro	Trp	Pro	Arg	Ala
															50
50															
55															60

Leu	Glu	Val	Asp	Ser	Arg	Ser	Val	Val	Leu	Leu	Ser	Val	Val	Trp	Val
														65	
65															
70															75

Leu	Leu	Ala	Pro	Pro	Ala	Ala	Gly	Met	Pro	Gln	Phe	Ser	Thr	Phe	His
															85
85															90

Ser	Glu	Asn	Arg	Asp	Trp	Thr	Phe	Asn	His	Leu	Thr	Val	His	Gln	Gly
															100
100															110

Thr	Gly	Ala	Val	Tyr	Val	Gly	Ala	Ile	Asn	Arg	Val	Tyr	Lys	Leu	Thr
															115
															120

Gly	Asn	Leu	Thr	Ile	Gln	Val	Ala	His	Lys	Thr	Gly	Pro	Glu	Glu	Asp
															130
															135

Asn	Lys	Ser	Arg	Tyr	Pro	Pro	Leu	Ile	Val	Gln	Pro	Cys	Ser	Glu	Val
															145
															150

Leu	Thr	Leu	Thr	Asn	Asn	Val	Asn	Lys	Leu	Leu	Ile	Ile	Asp	Tyr	Ser
															165
															170

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350  
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365  
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450                    455                    460  
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
465                    470                    475                    480  
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
485                    490                    495  
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
500                    505                    510  
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
515                    520                    525  
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
530                    535                    540  
Leu Tyr Phe Leu Gly Glu Gln Arg  
545                    550

<210> 171  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171  
tggaataaccg cctcctgcag

20

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172  
cttctgccct ttggagaaga tggc

24

<210> 173  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 173  
 ggactcactg gcccaggcct tcaatatac cagccaggac gat 42  
  
 <210> 174  
 <211> 3106  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> modified\_base  
 <222> (1683)  
 <223> a, t, c or g  
  
 <400> 174  
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 aacacgcgt gaccacgtgg agcctccggc ggaggccggc ccccacgtcg ggactccctgc 120  
 tgctggctgt ctggggttc ctgggtctcc gcaggctgga ctggagcacc ctggccctc 180  
 tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240  
 attccaccc ttggatcttc gggggctcca tccactattt ccgtgtgcc agggagtact 300  
 ggagggacccg cctgtgaag atgaaggcct gtggctgaa caccctcacc acctatgttc 360  
 cgtggAACCT gcatgagcca gaaagaggca aatttgactt ctctggaaac ctggacctgg 420  
 aggccttcgt cctgtatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggcccct 480  
 acatctgcag tgagatggac ctgggggctc tgccagctg gctactccaa gaccctggca 540  
 tgaggcttag gacaacttac aagggcttca ccgaagcagt ggaccccttat tttgaccacc 600  
 ttagtgtccag ggtggtgcca ctccagtaca agcgtgggg acctatcatt gccgtgcagg 660  
 tggagaatga atatggttcc tataataaaag accccgcata catgccctac gtcaagaagg 720  
 cactggagga ccgtggcatt gtggacttgc ttctgacttc agacaacaag gatggctga 780  
 gcaaggggat tggccaggga gtctggcca ccatcaactt gcagtcaaca cacgagctgc 840  
 agtactgac caccttttcc ttcaacgtcc aggggactca gcccaagatg gtatggagt 900  
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 caggtccctg gttgagcagc ggaatcaacc aggtcatgt ttttggggag acgtatggcgg 1920  
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 cgggtggcacc ccctcctgtt ggtgccagtg ggagactgccc gcctccctt gacgtggac 2040  
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 gaagtgtgtc caagtccgca ttgagccctt gttctgggc ccagcccaac acctggcttg 3060  
 ggctcactgt cctgagttgc agtaaagcta taacctgaa tcacaa 3106

&lt;210&gt; 175

&lt;211&gt; 636

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (539)

&lt;223&gt; Any amino acid

&lt;400&gt; 175

Met	Thr	Thr	Trp	Ser	Leu	Arg	Arg	Arg	Pro	Ala	Arg	Thr	Leu	Gly	Leu
1															15

Leu	Leu	Leu	Val	Val	Leu	Gly	Phe	Leu	Val	Leu	Arg	Arg	Leu	Asp	Trp
															30
20								25							

Ser	Thr	Leu	Val	Pro	Leu	Arg	Leu	Arg	His	Arg	Gln	Leu	Gly	Leu	Gln
															45
35							40								

Ala	Lys	Gly	Trp	Asn	Phe	Met	Leu	Glu	Asp	Ser	Thr	Phe	Trp	Ile	Phe
															50
50							55								

Gly	Gly	Ser	Ile	His	Tyr	Phe	Arg	Val	Pro	Arg	Glu	Tyr	Trp	Arg	Asp
															65
65					70				75						

Arg	Leu	Leu	Lys	Met	Lys	Ala	Cys	Gly	Leu	Asn	Thr	Leu	Thr	Thr	Tyr
															85
									90						

Val	Pro	Trp	Asn	Leu	His	Glu	Pro	Glu	Arg	Gly	Lys	Phe	Asp	Phe	Ser
															100
								105							

Gly	Asn	Leu	Asp	Leu	Glu	Ala	Phe	Val	Leu	Met	Ala	Ala	Glu	Ile	Gly
															115
								120							

Leu	Trp	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ser	Glu	Met	Asp
															130
								135							

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
 435 440 445  
 Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
 450 455 460  
 Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
 465 470 475 480  
 Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
 485 490 495  
 Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
 500 505 510  
 Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
 515 520 525  
 Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
 530 535 540  
 Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
 545 550 555 560  
 Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
 565 570 575  
 Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
 580 585 590  
 Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
 595 600 605  
 Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
 610 615 620  
 Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
 625 630 635  
 <210> 176  
 <211> 2505  
 <212> DNA  
 <213> Homo sapiens  
 <400> 176  
 ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60  
 ccctggtag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120  
 aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttgg 180  
 ggaatccgac acgtgacggt ctgtccgccc tctcagacta gaggagcgct gtaaacgcca 240  
 tggctcccaa gaagctgtcc tgctttcggt ccctgtcgct gccgctcagc ctgacgctac 300  
 tgctgccccca ggcagacact cggtcggtcg tagtgatag ggtcatgac cggttctcc 360  
 tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

tgctttggc cgaccggc ttgaagatgc gatggagcgg cctcaacgcc atacagttt 480  
 atgtgcctg gaactaccac gagccacagc ctgggtcta taacttaat ggcagccgg 540  
 acctcattgc ctttctaat gaggcagctc tagcAACCT gtggtcata ctgagaccag 600  
 gacccttacat ctgtcagag tggagatgg ggggtctccc atccctgttg cttegaaaac 660  
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctgttca 720  
 aggtcttgc gcccaagata tattccatggc tttatcacaa tgggggcaac atcattagca 780  
 ttcaggtgga gaatgaatat ggttagctaca gagcctgtga cttcagctac atgaggcact 840  
 tggctggcctt ccctcgta ctgtctaggag aaaagatctt gctcttcacc acagatggc 900  
 ctgaaggact caagtgtggc tccctccggg gactctatac cactgttagat tttggccag 960  
 ctgacaacat gaccaaatac tttaccctgc ttccgaagta tgaaccccat gggccattgg 1020  
 taaactctga gtactacaca gggtggctgg attactgggg ccagaatcac tccacacgg 1080  
 ctgtgtcagc tgtaacccaa ggactagaga acatgtcaa gttgggagcc agtgtgaaca 1140  
 tgtacatgtt ccatggaggt accaactttg gatattggaa tggtgccqat aagaaggac 1200  
 gcttccttcc gattactacc agtataact atgatgcacc tatatctgaa gcaggggacc 1260  
 ccacacctaa gcttttgc ttccgagatg tcatcagcaa gttccaggaa gttcccttgg 1320  
 gaccccttacc tccccccggc cccaaagatga tgcttgacc tggactctg cacctgggt 1380  
 ggcatttact ggcttceta gacttgctt gccccggg gcccattcat tcaatcttgc 1440  
 caatgacctt tgaggctgtc aagcaggacc atggctcat gttgtaccga acctatatga 1500  
 cccataccat ttttgagcca acaccattct ggggcacaaa taatggagtc catgaccgt 1560  
 cctatgtat ggtggatggg gtgttccagg gtgttgga gcgaaatatg agagacaaac 1620  
 tattttgac ggggaaactg gggtccaaac tggatatctt ggtggagaac atggggaggc 1680  
 tcagcttgg gtctaacagc agtacttca agggcctgtt gaagccacca attctgggc 1740  
 aaacaatctt taccctgtgg atgatgttcc ctctgaaaat tgataacctt gtgaagtgg 1800  
 ggtttccctt ccagttgcca aaatggccat atcctcaagc tccttctggc cccacattct 1860  
 actccaaaac atttccaatt ttaggctcag ttggggacac atttcttatat ctacctggat 1920  
 ggaccaaggc ccaagtctgg atcaatgggt ttaacttggg ccggactgtt acaaagcagg 1980  
 ggcacacaaca gaccctctac gtgccaagat tcctgtgtt tccttagggg gcccctaaca 2040  
 aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100  
 agcctatctt caatagact agtacttgc acaggacaca tatcaattcc ctttcagctg 2160  
 atacacttag tgcctctgaa ccaatgggt taatggggca ctgaaaaggta ggcgggcat 2220  
 ggtggctcat gcctgtatac ccagcacttt gggaggtgtt gacgggtggg ttacctgagg 2280  
 tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340  
 aaatttagccg ggcgtgtatgg tgggcacctc taatccacg tacttggag gctgagggca 2400  
 ggagaattgc ttgaatccag gaggcagagg ttgcagttag tgaggttgtt accactgcac 2460  
 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

<210> 177  
 <211> 654  
 <212> PRT  
 <213> Homo sapiens

<400> 177  
 Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
 1 5 10 15

Ser Leu Thr Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Val Asp Phe Gly Pro  
 225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
560		
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179

tggacaaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182  
 tggcacccag aatgggtttg gctc 24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttggac cttaacctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 gcttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60  
 gcacccacaa tatggcttac atgttggaaaa agtttcata cagttacata tccattattt 120  
 gtgttatgg ctatctgc ctctacactc ttctctggtt attcaggata ccttgaagg 180  
 aatattctt cggaaaagtc agagaagaga gcaagtttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagttatga ccagctataat tccaagcggt 300  
 ttgggtgttt cttgtcagaa gtttgtgaaa ataaaacttag gggaaatttagt ttgaaccatgt 360  
 agtggacatt tgaaaaactc aggccgacaa ttccacgcaa cggccaggac aagcaggagt 420  
 tgcattctgtt catgctgtcg ggggtgcccgg atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattctgc taagattct caaatgacta 540  
 accttcaaga gctccacactc tgccactgccc ctgcaaaaat tgaacagact gcttttagct 600  
 ttcttcgcga tcacttgaga tgcccttacg tgaagttcac tggatgtggct gaaattctgt 660  
 cctgggtgtt tttgtcaaaa aacccctcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgataatg cttgaatctc tccggagatg gccggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagtccctt ccaacattac agatgtggct ccacatctta 840  
 caaagtttagt cattcataat gacggcacta aactcttggt actgaacacgc cttaagaaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 950  
 ttttcagctt ctcttaattt caggaactgg atttaaagtca caataacattt cgcacaattt 1020  
 aggaaatcat cagtttccag cattttaaac gactgacttg tttaaaaatta tggcataaca 1080  
 aaattgttac tattccccc tctattaccc atgtcaaaaa ctggagatca cttaattttct 1140  
 ctaacaacaa gctcgaatcc ttaccaggatgg cagtttttagt ttacagaaaa ctcagatgtct 1200  
 tagatgttagt ctacaacaaat tttcaataga aataggattt cttcagaacc 1260  
 tgcagcattt gcatatcact ggaaacaaatg tggacattctt gccaaaacaaat ttgtttaat 1320

gcataaaagtt gaggacttg aatctggac agaactgcat cacctcaactc ccagagaaaag 1380  
 ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttgc gaccgcctgc 1440  
 cagccccagct gggccaggtgt cgatgctca agaaaagcg ggcttgggtg gaagatcacc 1500  
 tttttgatac cctgccactc gaagtcaaag aggcatggaa tcaagacata aatattccct 1560  
 ttgcaaatgg gattnaaact aagataatat atgcacagtgc atgtgcagga acaacttcct 1620  
 agattgcaag tgctcacgtca caagttttaa caagataatg catttttagga gtagatatacat 1680  
 cttttaaaat aaaacagaga ggatgcata gaggctgata gaagacataa ctgaatgttc 1740  
 aatgtttgtt gggtttaag tcatttcattt ccaaattttt ttttttttgc ttttggggaa 1800  
 agggaaaggaa aaattataat cactaatctt ggttctttt aaattgtttg taacttggat 1860  
 gctgccgcta ctgaatgttt acaaattgtctt ggcctgctaa agttaatgtat taaattgaca 1920  
 ttttcttact aaaaaaaaaaaaaaaa 1947

&lt;210&gt; 185

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

Met	Ala	Tyr	Met	Leu	Lys	Lys	Leu	Leu	Ile	Ser	Tyr	Ile	Ser	Ile	Ile
1															

5

10

15

Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg

20

25

30

Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser

35

40

45

Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His

50

55

60

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe

65

70

75

80

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His

85

90

95

Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln

100

105

110

Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala

115

120

125

Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro

130

135

140

Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu

145

150

155

160

Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser

165

170

175

Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val

180

185

190

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465

470

475

480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro  
 485 490 495

Phe Ala Asn Gly Ile  
 500

&lt;210&gt; 186

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 186

cctccctcta ttacccatgt c

21

&lt;210&gt; 187

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 187

gaccaacttt ctctggagt gagg

24

&lt;210&gt; 188

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 188

gtcactttat ttctctaaca acaagctcgaa atccttacca gtggcag

47

&lt;210&gt; 189

&lt;211&gt; 2917

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

ccccacgcgtc cggccttctc tctggacttt gcatttccat tcctttcat tgacaaaactg 60  
 actttttta tttcttttt tccatctcg ggccagcttg ggatcctagg ccgcctggg 120  
 aagacatttg tgtttacac acataaggat ctgtgtttgg ggtttcttct tcctcccctg 180

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565

570

575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe  
 580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr  
 595 600 605

&lt;210&gt; 191

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 191

tctctattcc aaactgtggc g

21

&lt;210&gt; 192

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 192

tttgatgacg attcgaaggt gg

22

&lt;210&gt; 193

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc

47

&lt;210&gt; 194

&lt;211&gt; 2362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

gacggaagaa cagcgctccc gagggccgcgg gagcctgcag agaggacagc cggcctgcgc 60  
 cgggacatgc ggccccagga gctccccagg ctcgcgttcc cgttgctgtct gttgctgttg 120  
 ctgctgctgc cgccgcccgttgc cacagcgcca cgcgcgttca cccccacctgg 180

gagtccttgg acgcccgcga gctgcccccg 240  
atccactggg gagtgtttc cgtccccagc ttccggtagcg agtgggtctg gtggatttgg 300  
caaaaaggaaa agataccgaa gatatgtggaa ttatgaaag ataattaccc tccttagttc 360  
aaatatgaag attttggacc actattaca gaaaaatttt ttaatgccaa ccagtggcca 420  
gatattttc aggccctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480  
tttaccttgt ggggttcaga atattgtgg aactggaatg ccataagatg ggggccc 540  
agggacattg tcaaggaact tgaggttagcc attaggaaca gaactgaccc gcgttttgg 600  
ctgtactatt cccttttga atggttcat ccgccttcc ttgaggatga atccagttca 660  
ttccataagg ggcattttcc agtttctaag acattgcccag agctctatga gtttagtgaac 720  
aactatcagc ctgaggttct gtggcggat ggtgacggag gggcc 780  
aacagcacag gcttcttggc ctggttatataatgaaagcc cagttcgggg cacagtagtc 840  
accaatgatc gttggggagc tgtagcata tgtaagcatg gtggcttcta tacctgcagt 900  
gatcgttata acccaggaca tcttttgcata cataaatggg aaaactgcata gacaatagac 960  
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caaacgtttt aatttttaaa accttttgg ctctttgttataacactta gcttaaaaaca 2340  
taaactcatt gtgcaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu  
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Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr  
20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala  
35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
 450 455 460

Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cggt

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197

ggatttcatcc tcaaggaaaga gcgg

24

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe  
  
 <400> 198  
 aacttgcagc atcagccact ctgc 24  
  
 <210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe  
  
 <400> 199  
 ttccgtgccc agcttcggta gcgagtggtt ctgggtggat tggca 45  
  
 <210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 200  
 agcaggaaaa tccggatgtc tcggtttatga agtggagcag tgagtgtgag cctcaacata 60  
 gttccagaac tctccatccg gacttagttat tgagcatctg cctctcatat caccagtggc 120  
 catctgaggt gttccctgg ctctgaaggg gtggcacgaa tgcccgaggta cttcagccctg 180  
 gtgttgcctc tcacttccat ctggaccacg aggctcctgg tccaaggctc tttgcgtgca 240  
 gaagagctt ccattccaggta gtcatgcaga attatgggta tcacccttgc gagcaaaaag 300  
 gccaaccaggc agctgaattt cacagaagct aaggaggccct gtaggctgc gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctgggttg gagatggatt cgtggtcata tctaggatta gcccaaacc caagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttggaaag gttccagtga gccgacagtt tgcagccat 540  
 tggttacaact catctgatac ttggactaac tcgtgcattc cagaattt caccaccaaa 600  
 gatccccat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgacagt 660  
 acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tccctctgct 720  
 ccagcttcca cttcttatcc acggagaaaa aaattgattt gtgtcacaga agttttatg 780  
 gaaaactagca ccatgtctac agaaaactgaa ccatttggta aaaataaagc agcattcaag 840  
 aatgaagctg ctgggtttgg aggtgtcccc acggctctgc tagtgcgtgc tctcccttc 900  
 tttgggtgtc cagctggctc tggattttgc tatgtcaaaa ggtatgtgaa ggccttcct 960  
 tttacaaaca agaatcagca gaaggaaatg atcgaacca aagttagtaaa ggaggagaag 1020  
 gccaatgata gcaaccctaa tgaggaatca aagaaaaactg ataaaaaacc agaagagtcc 1080  
 aagagtccaa gcaaaaactac cgtgcgtatgc ctggaagctg aagtttagat gagacagaaaa 1140  
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 caaggagtca ctgagacaa ggcttctct actgattccg cagctcagac cctttttca 1560  
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 cactgtttag aacacacaca cttactttt ctggctctca ccactgctga tattttctct 1860  
 aggaaaatata cttttacaag taacaaaaat aaaaactctt ataaatttct attttatct 1920  
 gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980  
 ttcaacaaac atttgctgaa tagtactat atgtcaagtg ctgtgcaagg tattacactc 2040  
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 atacctaaga agtacattgt tacctctata taccaaagca cattttaaaa gtgccattaa 2280  
 caaatgtatc actagccctc cttttccaa caagaaggaa ctgagagatg cagaaatatt 2340  
 tgtgacaaaaa aattaaagca ttttagaaaaac tt 2372

&lt;210&gt; 201

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Synthetic protein

&lt;400&gt; 201

Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Thr	Ile	Trp	Thr
1														15

Thr	Arg	Leu	Leu	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile
															30
20								25							

Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala
															45
35								40							

Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu
															60
50								55							

Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala
															80
65								70							

Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val
															95
85								90							

Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly
															110
100								105							

Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys
															125
115								120							

Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile
															140
130								135							

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 202  
 gagcttcca tccaggtgtc atgc 24

<210> 203  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203  
gtcagtgaca gtacctactc gg

22

<210> 204  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204  
tggaggcagga ggagtagtag tagg

24

<210> 205  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 205  
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206  
<211> 1620  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (973)  
<223> a, t, c or g

<220>  
<221> modified\_base  
<222> (977)  
<223> a, t, c or g

<220>  
<221> modified\_base  
<222> (996)  
<223> a, t, c or g

<220>  
<221> modified\_base

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

agatggcggt cttggcacct ctaattgctc tcgtgttattc ggtgccgcga ctttcacat 60  
 ggctcgccca accttactac ctctgtcgg ccctgtctc tgctgccttc ctactcgtga 120  
 gaaaaactgcc gccgctctgc cacggctctgc ccacccaacg cgaagacggg aaccctgtg 180  
 actttgactg gagagaagtg gagatcctga tgtttcttag tgccattgtg atgatgaaga 240  
 accgcagatc catcactgtg gagaacata taggaacat ttcatgttt agtaaagtgg 300  
 ccaacacaat tctttcttc cgcttggata ttgcgtatggg cctactttac atcacactct 360  
 gcatagtgtt cctgatgacg tgcaaaccaccc ccctatatat gggcccttag tatataagt 420  
 acttcaatga taaaaccatt gatgaggaac tagaacgggaa caagagggtc acttggattg 480  
 tggagttctt tgccaattgg tctaattgact gccaatcatt tgcccctatac tatgtctgacc 540  
 tctccctaa atacaactgt acagggctaa attttggaa ggtggatgtt ggacgctata 600  
 ctgatgttag tacgcgtac aaagttagca catcacccct caccaggcaaa ctccctaccc 660  
 tgatctgtt ccaaggtggc aaggaggcaaa tgccggcc acagattgac aagaaaggac 720  
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 tttctccatg aaactctgtg gttcatcat tccttcttag ttgacctgca cagcttggtt 1260  
 agaccttagat ttaaccctaa ggttaagatgc tgggtatag aacgctaaga atttcccc 1320  
 aaggacttt gttccctaa gccctctgg ctgcgttat ggtcttcatt aaaagtataa 1380  
 gcctaacttt gtcgttagtc ctaaggagaa accttaacc acaaagttt tattcattgaa 1440  
 gacaatattt aacaacccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500  
 acttccttt gtgtggtagg acttggagga gaaatccctt ggactttcac taaccctctg 1560  
 acatactccc cacaccctgt ttagggcttt ccgtataaaa aagattgggaa tttccctttt 1620

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1 5 10 15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65 70 75 80



<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 211  
 ccatgtatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
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 cccattgttc ctgtctggccg gcttctacgg actgccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240  
 gaagctggtg gtggagacac cggaggagac cctgttcacc taccaagggg ccagtgtgat 300  
 cctgccttc cgctaccgct acgagccggc cctggcttcc cccggcggtg tgcgtgtcaa 360  
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 gaggcaccgc tcctttgggg actaccaagg cccgtgcac ctgcggcagg acaaagagca 480  
 tgaacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540  
 ggtcattgac gggctggagg atgaaagcgg tctgggtggag ctggagctgc ggggtgtgg 600

ctttccttac cagtcccca acggcgcta ccagttcaac ttccacgagg gccagcaggt 660  
 ctgtcagag caggctgcgg tggggcctc ctttgagcag ctcttcggg cctggagga 720  
 gggctggac tggtcaacg cggctggct gcaggatgt acggtgcagt accccatcat 780  
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 ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggctgcca 960  
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 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1980  
 aaaaaa 1985

&lt;210&gt; 213

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 213

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr

1

5

10

15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp

20

25

30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys

35

40

45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala

50

55

60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
65 70 75 80Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
85 90 95Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr		
130	135	140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu		
145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg		
165	170	175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala		
180	185	190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly		
195	200	205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr		
210	215	220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro		
225	230	235
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp		
245	250	255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu		
260	265	270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu		
275	280	285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys		
290	295	300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser		
305	310	315
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu		
325	330	335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr		
340	345	350
Gly Val Tyr Cys Tyr Arg Gln His		
355	360	
<210> 214		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215

tccaccttgtg ggttggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216

aggcgtggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217

agccagttag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218

tgtccaaagt acacacacacct gagg

24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
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 tggccagggg agggtgcacc aggccggccc cctgagcgac gctccccatg atgacgccc 180  
 cgggaacttc cagtacgacc atgaggctt cctggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccg tctggggcgg atcgtggacc goatggaccg 300  
 cgcggggac ggcgacggct ggggtgcgct ggcgcgactt cgccgcgtgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcggtgag cgccgcctgg gacacgtacg acacggaccg 420  
 cgacggcgt gtggggttggg aggagctgca caacgcacc tatggccact acgcgcccgg 480  
 tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctgggacga 540  
 goggcgtttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600  
 agccttcctg caccggcagg agttccctca catgcgggac atcgtgattt ctgaaaccct 660  
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 gtactcagcc gagcctgggg aggaggagcc ggctgggtg cagacggaga ggcagcagtt 780  
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 ccagggaggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagctcc 1260  
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 cagctccaaa tctgagcctc caccacatag actgaaactc ccctggcccc agccctctcc 1380  
 tgcctggcct ggcctggac acctcctctc tgccagagg caataaaagc cagcggccgg 1440  
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
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Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala			
35	40	45	
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val			
50	55	60	
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu			
65	70	75	80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp			
85	90	95	
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg			
100	105	110	
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp			
115	120	125	
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly			
130	135	140	
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr			
145	150	155	160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp			
165	170	175	
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu			
180	185	190	
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr			
195	200	205	
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu			
210	215	220	
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Pro Ala			
225	230	235	240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn			
245	250	255	
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro			
260	265	270	
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu			
275	280	285	

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<210> 227

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

Met	Ser	Ala	Ala	Trp	Ile	Pro	Ala	Leu	Gly	Leu	Gly	Val	Cys	Leu	Leu
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Leu	Leu	Pro	Gly	Pro	Ala	Gly	Ser	Glu	Gly	Ala	Ala	Pro	Ile	Ala	Ile
														30	
20							25								

Thr	Cys	Phe	Thr	Arg	Gly	Leu	Asp	Ile	Arg	Lys	Glu	Lys	Ala	Asp	Val
														45	
35							40								

Leu	Cys	Pro	Gly	Gly	Cys	Pro	Leu	Glu	Glu	Phe	Ser	Val	Tyr	Gly	Asn
														60	
50							55								

Ile	Val	Tyr	Ala	Ser	Val	Ser	Ser	Ile	Cys	Gly	Ala	Ala	Val	His	Arg
														80	
65							70								

Gly	Val	Ile	Ser	Asn	Ser	Gly	Gly	Pro	Val	Arg	Val	Tyr	Ser	Leu	Pro
														95	
85								90							

Gly	Arg	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ala	Asn	Gly	Ile	Gln	Ser	Gln
														110	
100								105							

Met	Leu	Ser	Arg	Trp	Ser	Ala	Ser	Phe	Thr	Val	Thr	Lys	Gly	Lys	Ser
														125	
115								120							

Ser	Thr	Gln	Glu	Ala	Thr	Gly	Gln	Ala	Val	Ser	Thr	Ala	His	Pro	Pro
														140	
130							135								

Thr	Gly	Lys	Arg	Leu	Lys	Thr	Pro	Glu	Lys	Lys	Thr	Gly	Asn	Lys
														160
145							150							

Asp	Cys	Lys	Ala	Asp	Ile	Ala	Phe	Leu	Ile	Asp	Gly	Ser	Phe	Asn	Ile
														175	
165								170							

Gly	Gln	Arg	Arg	Phe	Asn	Leu	Gln	Lys	Asn	Phe	Val	Gly	Lys	Val	Ala
														190	
180								185							

Leu	Met	Leu	Gly	Ile	Gly	Thr	Glu	Gly	Pro	His	Val	Gly	Leu	Val	Gln
														205	
195							200								

Ala	Ser	Glu	His	Pro	Lys	Ile	Glu	Phe	Tyr	Leu	Lys	Asn	Phe	Thr	Ser
														220	
210							215								

Ala	Lys	Asp	Val	Leu	Phe	Ala	Ile	Lys	Glu	Val	Gly	Phe	Arg	Gly	Gly
														240	
225							230				235				

Asn	Ser	Asn	Thr	Gly	Lys	Ala	Leu	Lys	His	Thr	Ala	Gln	Lys	Phe	Phe
														255	
245							250								

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270  
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285  
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335  
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350  
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415  
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445  
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480  
 Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510  
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
 515 520 525  
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228  
tggtctcgca caccgatc

18

<210> 229  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229  
ctgctgtcca caggggag

18

<210> 230  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230  
ccttgaagca tactgctc

18

<210> 231  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231  
gagatagcaa ttccgc

18

<210> 232

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 232  
 ttccctcaaga gggcagcc 18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga ttcc 24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 234  
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
 cgccgcgcgc ccgcacccgc ggccccccca ccgcgcgcgt cccgcacatctg cacccgcagc 60  
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 gtccggggcggt cggctcgccc cgcagagcggt agatgcagcg gcttggggcc accctgtgt 180  
 gcctgctgtt ggcggcgccg gtcccccacgg ccccccgcgc cgcgtccgcacg ggcaccccg 240  
 ctccaggtaa gccccggcccg gctctcagct acccgacgga ggaggccacc ctcaatgaga 300  
 tggccgcga ggttgaggaa ctgtatggagg acacgcacgca caaatgcgc agcgcgggtgg 360  
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc aagaagtgaac ctggcaaact 420  
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaaat aataccatcc 480  
 atgtgcacccg agaaaattcac aagataacca acaaccacgac tggacaaaatg gtctttcag 540  
 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcg 600  
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taaagttgca catgattgtt taagcatgt ttctttgagt tttaaattat gtataaaccat 2520  
aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaaaa aaaaaaaaaaa 2580  
aaaaaaaaa 2586

<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala  
1 5 10 15

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80



<211> 17	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide probe	
<400> 237	17
ggagctgcac cccttgc	
<210> 238	
<211> 49	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	
<400> 238	49
ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg	
<210> 239	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	
<400> 239	24
gcagagcgg aatgcagcgg cttg	
<210> 240	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	
<400> 240	18
ttggcagctt catggagg	
<210> 241	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic Oligonucleotide Probe	
<400> 241	18
cctggcaaa aatgcaac	

<210> 242  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgcacct cctc 24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg 45

<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

<400> 244  
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 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met  
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 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg  
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Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu		
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Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
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Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
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Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
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Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
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Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
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Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
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Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
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Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
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Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
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Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
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Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly		
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Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
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Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
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Leu Pro Pro Leu Ser Gln Asn Ser  
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<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 246

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<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

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<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

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catcaagtgc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200  
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 a 3401

&lt;210&gt; 250

&lt;211&gt; 546

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 250

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Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
														30
									20		25			

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
														45
					35				40					

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
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									50		55			

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
														75
					65				70					

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
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									80		85			

Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys
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140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
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Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
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Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
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Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
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245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
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Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
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Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
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Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
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Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
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Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
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Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
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Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
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Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
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Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
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Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
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Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
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Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
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Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
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Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
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&lt;210&gt; 251

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

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&lt;210&gt; 252

&lt;211&gt; 24

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<210> 254  
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<212> DNA  
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 tcgtagatac catgggtcag gaggcctggg tgcgaaaact gaagtggcca 1200  
 gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250  
 taaatcttg gaaacatctg ctttgcctaa gtcctacaag aaccttgctt 1300  
 tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350  
 atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400  
 gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450  
 cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500  
 gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550  
 ggaggcaatt tggaaattat ttctgcttct taaaaaaaaacc taagatttt 1600  
 taaaaaaaaatg atttgttttgc atcaaaataa aggatgataa tagatattaa 1650

&lt;210&gt; 255

&lt;211&gt; 452

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1														15
Leu	Leu	Pro	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp	
														30
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
														45
35														

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn  
                   50                      55                      60  
 Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln  
                   65                      70                      75  
 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu  
                   80                      85                      90  
 Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp  
                   95                      100                    105  
 Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr  
                   110                      115                    120  
 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu  
                   125                      130                    135  
 Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe  
                   140                      145                    150  
 Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser  
                   155                      160                    165  
 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu  
                   170                      175                    180  
 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly  
                   185                      190                    195  
 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu  
                   200                      205                    210  
 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys  
                   215                      220                    225  
 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala  
                   230                      235                    240  
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys  
                   245                      250                    255  
 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr  
                   260                      265                    270  
 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser  
                   275                      280                    285  
 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His  
                   290                      295                    300  
 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp 320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe 335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly 350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp 365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu 380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp 395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn 410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser 425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln 440	445	450
Gln Glu		

&lt;210&gt; 256

&lt;211&gt; 1100

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 256

ggccgcggga gaggaggcca tggcgcgcg cggggcgctg ctgctggcgc 50

tgctgctggc tcgggctgga ctcaggaagc cggagtgcga ggaggcggcg 100

ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctggca 250

ctcacggcgg cgcaactgctt tgaaacctat agtgcaccta gtgatccctc 300

cggtggatg gtccagttg gccagctgac ttccatgcca tccttctgga 350

gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

cctcgctacc tgggaaattc accctatgac attgccttgg tgaagctgtc 450  
 tgcacctgtc acctacacta aacacatcca gccccatctgt ctccaggcct 500  
 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550  
 tacatcaaag aggatgaggc actgccatct ccccacaccc tccaggaagt 600  
 tcaggtcgcc atcataaaca actctatgtg caaccaccc ttcctcaagt 650  
 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700  
 caaggcggga aggatgcctg cttegggtgac tcaggtggac cttggcctg 750  
 taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800  
 gctgtggtcg gccaaatcgg cccgggtgtct acaccaatat cagccaccac 850  
 tttgagtgga tccagaagct gatggcccag agtggcatgt cccagccaga 900  
 cccctctgg ccactactt tttccctct tctctggct ctcccactcc 950  
 tggggccggt ctgagcctac ctgagccat gcagcctggg gccactgcca 1000  
 agtcaggccc tggttcttt ctgtcttgg tggtaataaa cacattccag 1050  
 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

&lt;210&gt; 257

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg
1					5				10				15	

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
													20	

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
										35			40	45

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
									50				55	60

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
									65				70	75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
									80				85	90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
                   95                     100                 105  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
                   110                    115                 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
                   125                    130                 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
                   140                    145                 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
                   155                    160                 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
                   170                    175                 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
                   185                    190                 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
                   200                    205                 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
                   215                    220                 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
                   230                    235                 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
                   245                    250                 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
                   260                    265                 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
                   275                    280                 285  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
                   290                    295                 300  
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
                   305                    310

<210> 258  
 <211> 2427  
 <212> DNA  
 <213> Homo Sapien

<400> 258  
 cccacgcgtc cgccggacgac tggaaaggac tccaaggctg 50

cctccttaggg ctctttgccc tcatcctctc tggcaa atgc agttac agcc 100  
cgagccccga ccagcggagg acgctgcccc caggctgggt gtcctggc 150  
cgtgcggacc ctgaggaaga gctgagtctc accttgc 200  
aatgtggaa agactctcg agctggtgca ggctgtgtcg gatcccagct 250  
ctcctaata cgaaaataac ctgaccctag agaatgtggc tcatctggtg 300  
aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggc 350  
cgagccccag aagtgcatt ctgtgatcac acaggactt ctgacttgc 400  
ggctgagcat ccgacaagca gagctgctgc tccctgggc tgagttcat 450  
caatatgtgg gaggacctac gaaaaacccat gttgttaagg ccccacatcc 500  
ctaccagctt ccacaggcct tggcccccata tgtggacttt gtggggggac 550  
tgccaccgttt tcccccaaca tcataccctga ggcaacgtcc tgagccgcag 600  
gtgacaggga ctgttaggcct gcatctgggg gtaacccct ctgtgatccg 650  
taagcgatac aacttgaccc cacaagacgt gggctctggc accagcaata 700  
acagccaagc ctgtgccag ttccctggagc agtatttcca tgactcagac 750  
ctggctcagt tcatacgccct cttcggtggc aactttgcac atcaggcatc 800  
atagccccgt gtggttggac aacaggccg gggccgggac gggattgagg 850  
ccagtctaga tgtgcagttac ctgatgagtg ctggtgccaa catctccacc 900  
tgggtctaca gtacccctgg ccggcatgag ggacaggagc cttccctgca 950  
gtggctcatg ctgctcagta atgagtca cctgcccacat gtgcatactg 1000  
ttagctatgg agatgatgag gactccctca gcagcgccta catccagccg 1050  
gtcaacactg agctcatgaa ggctgcccgt cggggctca ccctgcttt 1100  
cgccctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150  
agttccggccc tacctccct gcctccagcc cctatgtcac cacagtggga 1200  
ggcacatccct tccaggaacc tttccctcatc acaa atgaaa ttgttgacta 1250  
tatcagtgggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300  
aggaagctgt aacgaagttc ctgagctcta gcccccacct gccaccatcc 1350  
agttacttca atgccagtggtt ccgtgcctac ccagatgtgg ctgcacttcc 1400

tcatggctac tgggtggtca gcaacagagt gcccattcca tgggtgtccg 1450  
 gaacctcgcc ctctactcca gtgtttgggg ggatcctata cttgatcaat 1500  
 gagcacagga tccttagtgg ccgcggggc cttggcttcc tcaacccaag 1550  
 gctctaccag cagcatgggg caggtcttta tcatgttaacc cgtggctgcc 1600  
 atgagtcctg tctggatgaa gaggttagagg gccagggttt ctgctcttgt 1650  
 cctggctggg atcctgtaac aggctgggg aacccaactt cccagcttg 1700  
 ctgaagactc tactcaaccc ctgacccttt cctatcagga gagatggctt 1750  
 gtccccgtcc ctgaagctgg cagttcagtc ccttattctg ccctgttgaa 1800  
 agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aaccctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900  
 atcataactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950  
 gtaactagca tttttgaat gcctctccct ccgcatactca tctttctctt 2000  
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050  
 acttgatatt cattcccaa ttcactgcaa ggagacctct actgtcacccg 2100  
 ttactcttt cctaccctga catccagaaa caatggcctc cagtcatac 2150  
 ttctcaatct ttgctttatg gccttccat catagttgcc cactccctct 2200  
 ccttacttag cttccaggtc ttaacttctc tgactactct tgtcttcctc 2250  
 tctcatcaat ttctgtttct tcatggaatg ctgacccctca ttgtccatt 2300  
 tgttagattt tgctttctc agtttactca ttgtcccctg gaacaaatca 2350  
 ctgacatctca caaccattac catctacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaatg taaaaaa 2427

<210> 259  
 <211> 556  
 <212> PRT  
 <213> Homo Sapien

<400> 259  
 Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu  
 1 5 10 15  
 Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

20	25	30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu		
35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly  
 290 295 300  
 Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser  
 305 310 315  
 Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp  
 320 325 330  
 Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met  
 335 340 345  
 Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp  
 350 355 360  
 Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg  
 365 370 375  
 Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly  
 380 385 390  
 Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp  
 395 400 405  
 Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser  
 410 415 420  
 Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His  
 425 430 435  
 Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro  
 440 445 450  
 Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg  
 455 460 465  
 Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val  
 470 475 480  
 Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser  
 485 490 495  
 Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln  
 500 505 510  
 His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser  
 515 520 525  
 Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro  
 530 535 540  
 Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu  
 545 550 555

## Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

gcccgcgct ctctccggc gcccacacct gtctgagcgg cgca  
cgaggccgg gcgggctgct cggcgccgaa cagtgtcggt catggcagg 100

atccaggcc tcctcttcct tcttttctt ctgtctgtg ctgttggca 150

agtggccct tacagtgcctt octggaaacc cacttggcct gcataccgcc 200

tccctgtcggtt cttggccctt tctaccctca atttagccaa gccagacttt 250

ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300

taagggactt ccactgccccca ttacgaaga gccaagcaa tatctgtt 350

atgaaacgctt ctatgccaat ggccggcga cagagacgca ggtgggcattc 400

tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450

ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcagg 500

tcagcatttt tgggaaggac ttccctgtca actacccttt ctcaacatca 550

gtgaagttat ccacgggctg caccggcacc ctgggtggcag agaagcatgt 600

cctcacagctt gcccactgca tacacgtgg aaaaacctat gtgaaaggaa 650

cccagaagctt tcgagtgccc ttccctaaagc ccaagttaa agatggtggt 700

cgaggggcca acgactccac ttccatgtgg cccgagcaga tgaaattca 750

gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800

atgccaatga catcgccatg gattatgatt atgccttcctt ggaactcaaa 850

aagccccaca agagaaaattt tatgaagattt ggggtgagcc ctccctgtt 900

gcagctgcca gggggcagaa ttccatgtgg tggatgtacatc aatgaccgac 950

caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000

ttgctctacc agcaatgcga tgcccaagccca gggggccagcg ggtctgggt 1050

ctatgtgaggat atgtgaaaga gacagcagca gaagtggag cgaaaaattta 1100

ttggcattt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
 gatttcaacg tggctgtcag aatcactcct ctcaaatacg cccagattt 1200  
 ctattggatt aaaggaaact acctggattt tagggagggg tgacacagt 1250  
 ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagagg 1300  
 ccaaattgtt ttttgcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgt 1350  
 tgtgtgttaag gtgtcttata atctttacc tatttcttac aattgcaaga 1400  
 tgactggctt tactatttga aaactggttt gtgtatcata tcataatatca 1450  
 tttaaggcat ttgaaggcat acttttgcatt agaaaataaaa aaaatactga 1500  
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgttttg 1550  
 caaactttga ttttatttc atctgaactt gttcaaaga tttatattaa 1600  
 atatttggca tacaagagat atgaaaaaaaaaaaaaaa 1638

&lt;210&gt; 261

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Phe	Leu	Leu
1												15

Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
														30

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
														45

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Gl
														60

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
														75

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
														90

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile

95		100		105
----	--	-----	--	-----

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
														120

110		115
-----	--	-----

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser  
                  125                         130                         135  
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe  
                  140                         145                         150  
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val  
                  155                         160                         165  
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly  
                  170                         175                         180  
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu  
                  185                         190                         195  
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr  
                  200                         205                         210  
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys  
                  215                         220                         225  
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp  
                  230                         235                         240  
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro  
                  245                         250                         255  
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys  
                  260                         265                         270  
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp  
                  275                         280                         285  
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu  
                  290                         295                         300  
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala  
                  305                         310                         315  
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln  
                  320                         325                         330  
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp  
                  335                         340                         345  
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg  
                  350                         355                         360  
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly  
                  365                         370                         375  
 Asn Tyr Leu Asp Cys Arg Glu Gly  
                  380

<210> 262  
<211> 1378  
<212> DNA  
<213> Homo Sapien

<400> 262  
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ccatgggtt ttctggagcg ccccccagccc tgggtgggg ctgtctcgcc 100  
accttcacct ccctgctgtc gctggcgtcg acagccatcc tcaatgcggc 150  
caggataacct gttcccccag cctgtggaa gccccagcag ctgaaccggg 200  
tttgtggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
atccagaaga atgggaccca coactgcgc a gttctctgc tcaccagccg 300  
ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350  
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
cggtcccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450  
ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctgcagcgt 500  
ccatacagtt ctcagagcgg gtccctgccc tctgcctacc tgatgcctct 550  
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&lt;210&gt; 263

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 263

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Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
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Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
					50			55						60
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
					65					70				75
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
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Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
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Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
					110					115				120
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
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Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
					140					145				150
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
					155					160				165
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
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Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu  
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 Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His  
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 Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met  
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 Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly  
                  230                               235                     240  
 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu  
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 Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn  
                  260                               265                     270  
 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val  
                  275                               280                     285  
 Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly  
                  290                               295                     300  
 Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala  
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Arg Ser

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<220>  
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<400> 264  
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<210> 265  
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<220>  
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<400> 265  
 gcagaggtgt ctaaggttg 19

<210> 266  
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<212> DNA

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<220>

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<400> 266

agctctagac caatgccagg ttcc 24

<210> 267

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 267

gccaccaact cctgcaagaa ctttcagaa ctgcccctgg tcatg 45

<210> 268

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 268

gggaaattca ccctatgaca ttgcc 25

<210> 269

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 269

aatgccttg caagcatcaa ctgg 24

<210> 270

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

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gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

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gcggaaggc agaatggac tccaaag 26

<210> 272  
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<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
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<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
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<400> 274  
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<210> 277  
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<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
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<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
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<400> 279  
gcatcgatt gctggtagag caag 24

<210> 280  
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<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataaccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccataca gttcccttgc cccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

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tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttctgtat gtttctgtg 50

ccgctactgc tactgttgt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tggtggagct gcacaacctc taccgggccc 150  
aggatatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250  
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<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

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                   20                  25                          30

Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala  
35 40 45

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp  
50 55 60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val  
65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe  
80 85 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu  
95 100 105

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys  
110 115 120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala  
125 130 135



Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
440 445 450

Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
455 460

<210> 286

<211> 19

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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<210> 290  
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 <212> PRT  
 <213> Homo Sapien

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Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
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 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
                   50                        55                        60  
 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
                   65                        70                        75  
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
                   80                        85                        90  
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
                   95                        100                      105  
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
                   110                      115                      120  
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
                   125                      130                      135  
 Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
                   140                      145                      150  
 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn  
                   155                      160                      165  
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                   170                      175                      180  
 Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met  
                   185                      190                      195  
 Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu  
                   200                      205                      210  
 Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly  
                   215                      220                      225  
 Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn  
                   230                      235                      240  
 Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu  
                   245                      250                      255  
 Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser  
                   260                      265                      270  
 Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn  
                   275                      280                      285  
 Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser

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Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
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Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
545	550	555

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro  
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 Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro  
                   575                      580                  585  
  
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val  
                   590                      595                  600  
  
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser  
                   605                      610                  615  
  
 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr  
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 Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp  
                   635                      640                  645  
  
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala  
                   650                      655                  660  
  
 Gly Gly Ser Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser  
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 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
                   680                      685                  690  
  
 Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr  
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 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val  
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 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
                   725                      730                  735  
  
 Thr Ala Pro Ser Leu Asp Asp Gly Trp Ala Thr Val Gly Val  
                   740                      745                  750  
  
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
                   755                      760                  765  
  
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Asn Glu Asp Cys  
                   770                      775                  780  
  
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
                   785                      790                  795  
  
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
                   800                      805                  810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 815 820 825  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 860 865 870  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 890 895 900  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
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 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
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 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
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 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
 965 970 975  
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
 980 985 990  
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
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 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
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<213> Homo Sapien

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gaagctttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200  
acacagggag cattcaagaa taaaataaac cagagttaga cccgcgggg 250  
ttggtgtgtt ctgacataaa taaataatct taaaggcagct gttcccctcc 300  
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gatatttttgaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450  
ggtgtggtgg tgttttcctt tcttttggaa tttcccacaa gaggagagga 500  
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&lt;210&gt; 292

&lt;211&gt; 640

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
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Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
														30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
														45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
														60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
														75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
														90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
														105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
														120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
														135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
														150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

155	160	165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly		
170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly		
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg		
200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp		
215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln		
230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile		
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val		
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp		
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His		
290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp		
305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys		
320	325	330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp		
335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro		
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Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys		
365	370	375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn		
380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val		
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp		
410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
 425 430 435  
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
 440 445 450  
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
 455 460 465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
 470 475 480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
 485 490 495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
 500 505 510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
 515 520 525  
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
 530 535 540  
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
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 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
 560 565 570  
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
 590 595 600  
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
 605 610 615  
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
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 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
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&lt;210&gt; 293

&lt;211&gt; 4053

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 293

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<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met	Ser	Ala	Pro	Ser	Leu	Arg	Ala	Arg	Ala	Ala	Gly	Leu	Gly	Leu
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														30
20														

Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg
														45
35														

Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys
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50														

Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp
														75
65														

Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
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80														

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu
														105
95														

Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser
														120
110														

Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu
														135
125														

Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu
														150
140														

Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro
														165
155														

Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr
														180
170														

Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
														195
185														

Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys
														210
200														

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

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Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala		
230	235	240
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met		
245	250	255
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		
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275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		
305	310	315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser		
320	325	330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
350	355	360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
380	385	390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
440	445	450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
470	475	480

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 Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala  
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 Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu  
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 Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu  
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 Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn  
 575 580 585  
 His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn  
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 Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg  
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 Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro  
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 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr  
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 695 700 705  
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala  
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 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser  
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 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
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 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
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Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
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Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
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His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
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<400> 312  
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<211> 45  
<212> DNA  
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<400> 313  
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<210> 314  
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<212> DNA  
<213> Homo Sapien

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 Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys  
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 Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu  
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425	430	435
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Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly	440	445
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Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser	455	460
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465

Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala	470	475
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480

Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln	485	490
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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 316

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&lt;210&gt; 317

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;400&gt; 317

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&lt;210&gt; 318

&lt;211&gt; 50

&lt;212&gt; DNA

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&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

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&lt;210&gt; 319

&lt;211&gt; 2110

&lt;212&gt; DNA

<213> Homo Sapien

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agtaaccaag gaagacattt ggaattacag ctgcctgg(t)g aggaaccctg 700  
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aagatgaaac tcatttcaca gttatcatca cttccgttagg actggagaag 1050  
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agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050  
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210 <210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

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Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe  
35 40 45

His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg  
50 55 60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser  
                   65                     70                     75

Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro  
                   80                     85                     90

Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu  
                   95                     100                    105

Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu  
                   110                    115                    120

Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr  
                   125                    130                    135

Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr  
                   140                    145                    150

Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg  
                   155                    160                    165

Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser  
                   170                    175                    180

Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala  
                   185                    190                    195

Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg  
                   200                    205                    210

Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile  
                   215                    220                    225

Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu  
                   230                    235                    240

Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu  
                   245                    250                    255

Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp  
                   260                    265                    270

Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro  
                   275                    280                    285

Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp  
                   290                    295                    300

Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu  
                   305                    310                    315

Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
440	445	450

<210> 321  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 321  
gatcctgtca caaaggccagt ggtgc 25

<210> 322  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 322  
cactgacagg gttcctcacc cagg 24

<210> 323  
<211> 45  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 323

ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

&lt;210&gt; 324

&lt;211&gt; 2397

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50

cctggtgctg ttgcttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aatttatgc cccgtggtgc cctgcttgc aaaatcttca 200

accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gaggcagccag gactgagtg 300

ataactgctc ttcctactat ttatcattgt aaagatggc aattnaggcg 350

ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtgata 400

aagagtggaa gagtattgag cccgtttcat catggtttg tccaggttct 450

gttctgatga gtatgtatgc agcactctt cagctatcta tgtggatcag 500

gacgtgccat aactactta ttgaagaccc tggattgcca gtgtgggat 550

catatactgt ttttgcattt gcaactctgt tttccggact gttatttagga 600

ctctgtatga tatttgtggc agattgcctt tgtcattcaa aaaggcgcag 650

accacagcca tacccatacc cttcaaaaaa attattatca gaatctgcac 700

aaccttgaa aaaagtggag gaggaacaag aggccgatga agaagatgtt 750

tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800

gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850

cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900

aagattgatc atttgtttg gtttgaagtg aactgtgact ttttgaata 950

ttgcagggtt cagtctagat tgcattaaa ttgaagatgc tacattcaga 1000



aaaccttctt aaccacttca tttaagctga aaaaaaaaaaaa aaaaaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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														30
20									25					

Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
														45
35									40					

Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
														60
50									55					

Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
														75
65									70					

Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly
														90
80									85					

Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His
														105
95									100					

Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys
														120
110									115					

Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile
														135
125									130					

Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser
														150
140									145					

Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys
														165
155									160					

His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser
														180
170									175					

Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu
														195
185									190					

Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys
														210
200									205					

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

215

220

225

Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu  
230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Ala Glu Ser Lys Glu  
245 250 255

Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser  
260 265 270

Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser  
275 280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

tgaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 329  
ttgaaggaca aaggcaatct gccac 25

<210> 330  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 330  
ggagtcttgc agttcccttg gcagtcctgg tgctgttgt ttggg 45

<210> 331  
<211> 2168  
<212> DNA  
<213> Homo Sapien

<400> 331  
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aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taacccagtg 100  
ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150  
acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
ggtttgggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250  
cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300  
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gttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

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Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
				20					25					30

Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35					40				45

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50				55				60		

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65				70					75	

Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80				85					90	

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95				100					105	

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110				115					120	

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125				130					135	

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140				145					150	

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155				160					165	

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170				175					180	

Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185				190					195	

Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu
				200				205					210	

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg  
 215 220 225  
 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His  
 230 235 240  
 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu  
 245 250 255  
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu  
 260 265 270  
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro  
 275 280 285  
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys  
 290 295 300  
 Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His  
 305 310 315  
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu  
 320 325 330  
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met  
 335 340 345  
 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys  
 350 355 360  
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr  
 365 370 375  
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp  
 380 385 390  
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile  
 395 400 405  
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn  
 410 415 420  
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg  
 425 430 435  
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala  
 440 445 450  
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr  
 455 460 465  
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr  
 470 475 480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaatttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttctgtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaagaactcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 337  
gggcacatga ctgacacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338  
<211> 2789

<212> DNA  
<213> Homo Sapien

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agacaggaca atcttcttgg ggatgctgg cctggaaagcc agcgggcctt 200  
gctctgtctt tggcctcatt gaccccagggt tctctggta aaactgaaag 250  
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accatttct tgggtgaag gtcagcagc cggagttaga gtcacggta 2000  
cctggacga ggctggcctg gtcgcgtgtc cgagcagagg cccctccca 2050  
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<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro  
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Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg  
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Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala  
35 40 45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg  
50 55 60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr  
65 70 75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg  
80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val		
110	115	120
Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr		
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser		
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg		
155	160	165
His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile		
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu		
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala		
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly		
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg		
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro		
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly		
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu		
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu		
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr		
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr		
320	325	330
Ser Glu Ile Glu Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val		
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu		
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp  
 365 370 375  
 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala  
 380 385 390  
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp  
 395 400 405  
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro  
 410 415 420  
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg  
 425 430 435  
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu  
 440 445 450  
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg  
 455 460 465  
 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met  
 470 475 480  
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu  
 485 490 495  
 Leu Val Ala Glu Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe  
 500 505 510  
 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu  
 515 520 525  
 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp  
 530 535 540  
 Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg  
 545 550 555  
 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala  
 560 565 570  
 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro  
 575 580 585  
 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly  
 590 595 600  
 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp  
 605 610 615  
 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu  
 620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
 755 760 765  
 Gln Glu Gln Ala Asn Ser Thr  
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<210> 340  
 <211> 1572  
 <212> DNA  
 <213> Homo Sapien

<400> 340  
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 cttttgaag ggtgtatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tcttaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagttatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtcttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gttgagtca attaatatgg acacaaatga catgtggta atgatgagaa 450  
aagcttacaa atacgcctt gataagtata gagaccaata caactggtc 500  
ttccttgcac gccccactac gtttgcatac attgaaaacc taaagtattt 550  
tttgttaaaa aaggatccat cacagcctt ctatcttagc cacactataa 600  
aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
cagttgcct gaaatatgct ggagtattt cagaaaatgc agaagatgct 800  
gatggaaaag atgtatttaa taccaaatac gttggcttt ctattaaaga 850  
ggcaatgact tatcacccca accaggtgt agaaggctgt tggtcagata 900  
tggctgttac tttaatgga ctgactccaa atcagatgca tgtgatgatg 950  
tatgggtat accgccttag ggcatttggg catatttca atgatgcatt 1000  
ggtttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050  
agcgtgaata tgatcttgc ataggacgtg tggtgcatt attttagta 1100  
gtaactacat atccaataca gctgtatgtt tcttttctt ttctaatttgc 1150  
gtggcactgg tataaccaca cattaaagtc agtagtacat tttaaatgaa 1200  
gggtggtttt ttctttaaa acacatgaac attgtaaatg tggtggaaag 1250  
aagtgtttta agaataataa tttgcaaat aaactattaa taaatattat 1300  
atgtataaaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350  
tttgcgtatt ggtaaaaaaa tttaacagg tcttagcgt tctaagatatt 1400  
gcaaatgata tctctagttg tgaatttgcgt attaaagtaa aacttttagc 1450  
tgtgtgttcc cttaacttct aatactgatt tatgttctaa gcctccccaa 1500  
gttccaatgg atttgccttc tcaaaaatgta caactaagca actaaagaaa 1550  
attaaagtga aagttgaaaaa at 1572

<210> 341  
<211> 318  
<212> PRT  
<213> Homo Sapien

&lt;400&gt; 341

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					20				25					30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
					35				40					45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
					50				55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
					65				70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
					80				85					90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
					95				100					105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
					110				115					120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
					125				130					135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
					140				145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
					155				160					165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
					170				175					180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
										185				195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
									200		205			210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
					215				220					225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
									230		235			240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
									245		250			255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

260 265 270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln  
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly  
290 295 300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser  
305 310 315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaaagcc gttcttagacg cg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctgggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcgg tataaccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 346  
<211> 25  
<212> DNA  
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 346  
gggatgcagg tggtgtctca tgggg 25

<210> 347  
<211> 18  
<212> DNA  
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 347  
ccctcatgtta ccggctcc 18

<210> 348  
<211> 48  
<212> DNA  
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 348  
ggattctaat acgactcact atagggtca gaaaagcgca acagagaa 48

<210> 349  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349  
ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350  
<211> 48  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 350  
ggattctaat acgactcact atagggcggc gatgtccact ggggctac 48

<210> 351  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 351  
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<210> 352  
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<220>  
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<400> 352  
ggattctaat acgactcact atagggcacc cacgcgtccg gctgctt 47

<210> 353  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 353  
ctatgaaatt aaccctcact aaagggacgg gggacaccac ggaccaga 48

<210> 354  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 354  
ggattctaat acgactcact atagggcttg ctgcggttt tggccctg 48

<210> 355  
<211> 48

<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 355  
ctatgaaatt aaccctcact aaagggagct gccgatccca ctggatt 48

<210> 356  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 356  
ggattctaat acgactcact atagggcgga tcctggccgg cctctg 46

<210> 357  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 357  
ctatgaaatt aaccctcact aaagggagcc cgggcattgtt ctcagtta 48

<210> 358  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 358  
ggattctaat acgactcact atagggcgga aagatggcga ggaggag 47

<210> 359  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 359  
ctatgaaatt aaccctcact aaagggacca aggcacaaa cggaaatc 48

<210> 360  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 360  
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<210> 361  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 361  
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<210> 362  
<211> 47  
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<220>  
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<400> 362  
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<210> 363  
<211> 48  
<212> DNA  
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<220>  
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<400> 363  
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<210> 364  
<211> 47  
<212> DNA  
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<400> 364

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<210> 365  
<211> 48  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe  
  
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<210> 366  
<211> 48  
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<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 366  
ggattctaat acgactcact atagggcgca gcgatggcag cgatgagg 48  
  
<210> 367  
<211> 47  
  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 367  
ctatgaaatt aaccctcact aaagggacag acggggcaga gggagtg 47  
  
<210> 368  
<211> 47  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 368  
ggattctaat acgactcact atagggccag gagggcgtgag gagaaac 47  
  
<210> 369  
<211> 48  
<212> DNA  
<213> Artificial Sequence  
  
<220>

<223> Synthetic Oligonucleotide Probe

<400> 369  
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<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

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<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

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<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

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<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaaggagta agggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 374  
ggattctaat acgactcact atagggccag ctacccgcag gaggagg 47

<210> 375  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 375  
ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376  
<211> 997  
<212> DNA  
<213> Homo Sapien

<400> 376  
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agggagggag agaaaaaagag agagagagaa acaaaaaacc aaagagagag 100  
aaaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150  
tgcttccttt cccaaatgtt cttatggact gttgctggga tccccatct 200  
atttctcagt gcctgttca tcaccagatg tgttgtgaca tttagcatct 250  
ttcaaacctg tcatgagaaa aagtttcagc tacctgagaa ttccacagag 300  
cttcctcgct acaattatgg atcagggttca gtcaagaatt gttgtccatt 350  
gaactggaa tattttcaat ccagctgcta cttctttct actgacacca 400  
tttcctgggc gttaaagttta aagaactgct cagccatggg ggctcacctg 450  
gtggtatca actcacagga ggagcagggaa ttcctttct acaagaaaacc 500  
taaaatgaga gagttttta ttggactgtc agaccaggtt gtcgagggtc 550  
agtggcaatg ggtggacggc acaccttga caaagtctct gagttctgg 600  
gatgttagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650  
gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700  
tcaattatcc tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750

ggaaaatctc tttaagaaca gaaggcacaa ctcaaatgtg taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttg tactctgata caaataaaaa 900  
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 997

&lt;210&gt; 377

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 377

Met	Asn	Ser	Ser	Lys	Ser	Ser	Glu	Thr	Gln	Cys	Thr	Glu	Arg	Gly	
1									10				15		
Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro	
					20				25					30	
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	
					35				40					45	
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	
					50				55					60	
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	
					65				70					75	
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	
					80				85					90	
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	
					95				100					105	
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	
					110				115					120	
Gln	Glu	Gln	Glu	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	
					125				130					135	
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	
					140				145					150	
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	
					155				160					165	
Asp	Val	Gly	Glu	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
					170				175					180	

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
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Asn Pro Leu Asn Lys Gly Lys Ser Leu  
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<400> 384  
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<400> 385  
catcaagcgc ctctaccca 18

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<210> 393  
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<220>  
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<400> 394  
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<400> 403  
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<400> 405  
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<400> 419  
gggcctaacc ctcattacct tt 22

<210> 420  
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&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 420

tgtctgcctc agccccagga agg 23

&lt;210&gt; 421

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 421

tctgtccacc atcttgccctt g 21

&lt;210&gt; 422

&lt;211&gt; 3554

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 422

gggactacaa gccgcgccgc gctgccgctg gcccctcagc aaccctcgac 50

atggcgctga ggccggccacc gcgactccgg ctctgcgcgc ggctgcctga 100

cttcttcctg ctgctgcttt tcagggctg cctgataggg gctgtaaatc 150

tcaaattccag caatcgaacc ccagtggta aggaatttga aagtgtggaa 200

ctgtcttgcac tcattacgga ttccgcagaca agtgacccca ggatcgagtg 250

gaagaaaattt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300

ttcagggaga cttggcggtt cgtgcagaaa tactggggaa gacatccctg 350

aagatctgga atgtgacacg gagagactca gcccattatc gctgtgaggt 400

cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450

ctgtcaagt gaagccagtg acccctgtct gttagagtgcg gaaggctgta 500

ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550

ccggcctcac tacagcttgtt atcgcaatga tgtaccactg cccacggatt 600

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acaggcactt tggtgttcac tgctgttcac aaggacgact ctgggcagta 700

ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

agatggagt ctatgacctg aacattggcg gaattattgg gggggttctg 800  
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&lt;210&gt; 423

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 423

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Pro	Asp	Phe	Phe	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly	
				20				25				30		
Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
				35				40				45		
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
				50				55				60		
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Ile	Gln	Asp	Glu	Gln	Thr	
				65				70				75		
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly
				80				85				90		
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val
				95				100				105		
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg
				110				115				120		
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				125				130				135		
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
				140				145				150		
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly
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His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu
				170				175				180		
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe
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His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His  
200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala  
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu  
230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val  
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly  
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro  
275 280 285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly  
290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile  
305 310